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 Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn  
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 Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro  
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 Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr  
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 His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe  
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 Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile  
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 Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp  
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 Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly  
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Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile  
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Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala	
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Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu	
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Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp	Met	Ser	Arg	Leu	Ala	
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 Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu  
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 Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln  
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 Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu  
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 Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg  
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 Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp  
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 Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

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 Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met  
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 Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser  
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 Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile  
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 Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg  
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 Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val  
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&lt;210&gt; 339

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; FRXA02161

&lt;400&gt; 339

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gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa					835
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu					
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Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly	Tyr	Val	Pro	Leu	Gly					
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906

&lt;210&gt; 340

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 340

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Thr	Met	Leu	Ala	Gly	Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly
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Thr	Phe	Gly	Pro	Leu	Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu
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Arg	Gly	Val	Ile	Asp	Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg
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Val	Arg	Asp	Ala	Val	Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val
	130					135					140				

Asp	Ala	Leu	Ser	Ala	Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro
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Gly	Lys	Thr	His	Phe	Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln
				165					170					175	

Leu	Leu	Ala	His	Ala	Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg
			180					185					190		

Asp	Leu	Asp	Lys	Arg	Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu
		195					200					205			

Ala	Gly	Ser	Ser	Leu	Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu
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Gly	Phe	Asp	Ser	Ala	Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg
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 <223> FRXA02162

<400> 341

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Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
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Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
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Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
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Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
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tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 786  
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<210> 342

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 342

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Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met  
                   20                  25                  30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser  
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Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala  
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Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile  
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Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly  
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Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala  
                   100                  105                  110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg  
                   115                  120                  125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val  
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Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu  
   145                  150                  155                  160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val  
                   165                  170                  175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr  
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Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser  
                   195                  200                  205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg  
                   210                  215                  220



170								175				180				
cg	cc	ga	at	ac	ac	at	aa	at	aa	ga	cg	ag	ga	cg	gg	691
Arg	Pro	Gly	Ile	Thr	Thr	Ile	Lys	Ile	Lys	Gly	Arg	Ser	Glu	Arg	Gly	
			185						190				195			
at	aa	gc	tt	ga	ac	tg	gc	tt	ga	aa	tt	cc	ga	at	ga	739
Ile	Asn	Ala	Phe	Ala	Thr	Trp	Ala	Leu	Glu	Lys	Phe	Pro	Glu	Ile	Glu	
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gt	gt	gc	gt	ga	tct	ga	ga	ga	gt	gt	aa	ga	gc	ga	at	787
Val	Val	Ala	Val	Gly	Ser	Glu	Glu	Asp	Val	Val	Lys	Asp	Ala	Asp	Ile	
		215				220					225					
gt	at	gc	gc	ac	ac	ac	ga	gc	gc	gg	tcc	tcc	gc	tt	cc	835
Val	Ile	Ala	Ala	Thr	Thr	Thr	Asp	Ala	Ala	Gly	Ser	Ser	Ala	Phe	Pro	
		230			235					240					245	
ta	tt	aa	aa	ga	tg	ct	aa	cc	gg	gc	ga	tt	ct	ct	cc	883
Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala	Leu	Leu	Leu	Leu	Pro	
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gc	gc	gg	cg	tt	ga	ga	gc	ta	tt	ct	ga	ga	gc	cg	ct	931
Ala	Ala	Gly	Arg	Phe	Asp	Asp	Ala	Tyr	Leu	Leu	Asp	Asp	Ala	Arg	Leu	
			265					270					275			
gt	gt	ga	ta	at	gg	ct	ta	ga	gc	tg	ga	ga	ga	ta	gg	979
Val	Val	Asp	Tyr	Met	Gly	Leu	Tyr	Glu	Ala	Trp	Ala	Glu	Glu	Tyr	Gly	
		280					285					290				
cc	ca	gc	ta	ca	ct	ct	gg	at	cc	ga	ac	ca	tg	ta	ga	
Pro	Gln	Ala	Tyr	Gln	Leu	Leu	Gly	Ile	Pro	Gly	Thr	His	Trp	Tyr	Asp	
		295				300					305					
ct	gc	ct	ca	ga	aa	ct	ga	ct	ga	aa	at	tcc	ca	at	gg	
Leu	Ala	Leu	Gln	Gly	Lys	Leu	Asp	Leu	Ala	Lys	Ile	Ser	Gln	Ile	Gly	
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ga	at	tg	tcc	gg	aa	ct	ccc	ga	cg	ac	aa	ga	ga	ga	at	
Asp	Ile	Cys	Ser	Gly	Lys	Leu	Pro	Gly	Arg	Thr	Asn	Asp	Glu	Glu	Ile	
				330					335					340		
at	ct	ta	tcc	gt	gg	gg	at	cc	gt	ga	ga	gt	gc	tg	ga	
Ile	Leu	Tyr	Ser	Val	Gly	Gly	Met	Pro	Val	Glu	Asp	Val	Ala	Trp	Ala	
			345					350					355			
ac	ca	gt	ta	ga	aa	gc	ct	ga	aa	gg	gt	gg	ac	ac	tt	
Thr	Gln	Val	Tyr	Glu	Asn	Ala	Leu	Glu	Lys	Gly	Val	Gly	Thr	Thr	Leu	
		360					365					370				
aa	ct	tg	ga	ta	ccc	ga	ct	gc	tg	ga	ga	ga	aa	aa	aa	
Asn	Leu	Trp	Glu	Ser	Pro	Ala	Leu	Ala								
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<210> 344
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<213> Corynebacterium glutamicum
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Val	Asp	Val 35	Met	Glu	Glu	Thr	Leu 40	Val	Leu	Leu	Ala	Gln 45	Gly	Asp	Tyr
Lys 50	Met	Ala	Gly	Leu	Asn	Ser 55	Asn	Ser	His	Gly	Ala 60	Met	Ile	Thr	Phe
Pro 65	Glu	Asn	Pro	Glu	Phe 70	Glu	Gly	Met	Pro	Lys 75	Asp	Gly	Pro	Asp	Arg 80
Arg	Phe	Met	Ala	Met 85	Pro	Ala	Tyr	Leu	Gly 90	Gly	Arg	Phe	Lys	Asn 95	Thr
Gly	Val	Lys	Trp 100	Tyr	Gly	Ser	Asn 105	Ala	Glu	Asn	Lys	Ala	Ser 110	Gly	Leu
Pro	Arg	Ser 115	Ile	His	Thr	Phe	Val 120	Leu	Asn	Asp	Thr	Val 125	Thr	Gly	Ala
Pro 130	Lys	Ala	Ile	Met	Ser	Ala 135	Asn	Leu	Leu	Ser	Ala 140	Tyr	Arg	Thr	Gly
Ala 145	Val	Pro	Gly	Val	Gly 150	Val	Lys	His	Leu	Ala 155	Val	Ala	Asp	Ala	Thr 160
Thr	Leu	Ala	Val	Val 165	Gly	Pro	Gly	Val	Met 170	Ala	Lys	Thr	Ile	Thr 175	Glu
Ala	Cys	Ile	Ala 180	Glu	Arg	Pro	Gly	Ile 185	Thr	Thr	Ile	Lys	Ile 190	Lys	Gly
Arg	Ser	Glu 195	Arg	Gly	Ile	Asn	Ala 200	Phe	Ala	Thr	Trp	Ala 205	Leu	Glu	Lys
Phe 210	Pro	Glu	Ile	Glu	Val	Val 215	Ala	Val	Gly	Ser	Glu 220	Glu	Asp	Val	Val
Lys 225	Asp	Ala	Asp	Ile	Val 230	Ile	Ala	Ala	Thr	Thr 235	Thr	Asp	Ala	Ala	Gly 240
Ser	Ser	Ala	Phe	Pro 245	Tyr	Phe	Lys	Lys	Glu 250	Trp	Leu	Lys	Pro	Gly 255	Ala
Leu	Leu	Leu	Leu	Pro 260	Ala	Ala	Gly	Arg 265	Phe	Asp	Asp	Ala	Tyr	Leu	Leu

Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
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 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
 290 295 300  
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
 305 310 315 320  
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
 325 330 335  
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00219

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 Val Ala Arg Lys Lys  
 1 5  
 aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163  
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala  
 10 15 20  
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 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser  
 25 30 35  
 tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct 259  
 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser  
 40 45 50  
 cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307  
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg  
 55 60 65  
 tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca 355  
 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala  
 70 75 80 85  
 tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc 403  
 Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala

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Arg Tyr Phe Ala Asp Val Tyr Pro Gln Ser Arg Asn Thr Val Val Glu				
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ttg gat gca gag ctt gcc cgc ctg tcg cgt gaa tgg ttc gac att ccg				499
Leu Asp Ala Glu Leu Ala Arg Leu Ser Arg Glu Trp Phe Asp Ile Pro				
	120	125	130	
cgc gcg cca cgg gta aag att cgt gtg gat gat gcc cga atg gtg gca				547
Arg Ala Pro Arg Val Lys Ile Arg Val Asp Asp Ala Arg Met Val Ala				
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gaa tct ttc act ccc gca agc cgc gat gtg atc atc cgt gac gtt ttt				595
Glu Ser Phe Thr Pro Ala Ser Arg Asp Val Ile Ile Arg Asp Val Phe				
	150	155	160	165
gcc gga gct atc acg ccg cag aac ttc acc acc gtg gag ttc ttt gag				643
Ala Gly Ala Ile Thr Pro Gln Asn Phe Thr Thr Val Glu Phe Phe Glu				
	170	175	180	
cac tgt cac cgt ggc ctt gct ccc ggc gga ttg tac gtt gcc aac tgt				691
His Cys His Arg Gly Leu Ala Pro Gly Gly Leu Tyr Val Ala Asn Cys				
	185	190	195	
ggc gat cat tcg gat ctg cgc gga gct aaa tct gag ctc gcg gga atg				739
Gly Asp His Ser Asp Leu Arg Gly Ala Lys Ser Glu Leu Ala Gly Met				
	200	205	210	
atg gag gtg ttc gag cac gtc gcg gtc atc gcc gat ccc ccg atg ctt				787
Met Glu Val Phe Glu His Val Ala Val Ile Ala Asp Pro Pro Met Leu				
	215	220	225	
aaa ggg cgc cgt tac ggc aac atc att ttg atg ggt tca gac acc gag				835
Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met Gly Ser Asp Thr Glu				
	230	235	240	245
ttc ttt agc tcc aac agc acg gaa gcg tcc gcg att acc cgt gag ctt				883
Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala Ile Thr Arg Glu Leu				
	250	255	260	
ctt ggc ggc ggc gtt cca gcg cag tac aag gat gaa tcc tgg gtg cgg				931
Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp Glu Ser Trp Val Arg				
	265	270	275	
aaa ttc gcc tcg gga gcc cag gcc cgc cac gat ggg gtc tct acc ctc				979
Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp Gly Val Ser Thr Leu				
	280	285	290	
caa atg ccg agt gat act cca caa cac cct gcg gaa acg ccg gag cat				
1027				
Gln Met Pro Ser Asp Thr Pro Gln His Pro Ala Glu Thr Pro Glu His				
	295	300	305	
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Ser Asn Thr Gln Pro				
310				

<210> 346  
 <211> 314  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 346

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			20					25					30		
Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn
		35					40					45			
Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu
	50					55					60				
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp
65					70					75					80
Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly
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Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg
			100					105					110		
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu
		115					120					125			
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp
	130					135					140				
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile
145					150					155					160
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr
				165					170					175	
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu
			180					185					190		
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser
		195					200					205			
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala
	210					215					220				
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met
225					230					235					240
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala
				245					250					255	
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp
			260				265						270		
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp
		275					280					285			
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
	310	315	320	325
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
1171				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu  
 375 380 385  
 ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg  
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 Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val  
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 1363  
 Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val  
 410 415 420  
 gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac  
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 Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His  
 425 430 435  
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 1459  
 Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro  
 440 445 450  
 gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc  
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 Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe  
 455 460 465  
 ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat  
 1555  
 Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn  
 470 475 480 485  
 cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg  
 1603  
 Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val  
 490 495 500  
 gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac  
 1649  
 Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp  
 505 510  
 gatgcgctgt gtg  
 1662

&lt;210&gt; 348

&lt;211&gt; 513

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 348

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 20 25 30  
 Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile  
 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys  
 50 55 60  
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu  
 65 70 75 80  
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe  
 85 90 95  
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala  
 100 105 110  
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile  
 115 120 125  
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala  
 130 135 140  
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala  
 145 150 155 160  
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala  
 165 170 175  
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val  
 180 185 190  
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val  
 195 200 205  
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser  
 210 215 220  
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val  
 225 230 235 240  
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg  
 245 250 255  
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr  
 260 265 270  
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn  
 275 280 285  
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala  
 290 295 300  
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu  
 305 310 315 320  
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp  
 325 330 335  
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp  
 340 345 350  
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp  
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg  
 370 375 380  
 Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu  
 385 390 395 400  
 Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp  
 405 410 415  
 Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln  
 420 425 430  
 Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe  
 435 440 445  
 Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr  
 450 455 460  
 Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val  
 465 470 475 480  
 Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp  
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Asp

<210> 349  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(901)  
 <223> RXA01757

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 Met Pro Thr Ala Ser  
 1 5  
 cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163  
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile  
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 gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211  
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu  
 25 30 35  
 gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259  
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp  
 40 45 50  
 ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu	
55						60					65					
gtg	cag	caa	ctc	gtc	aat	aat	ctc	ggc	ctc	ggc	aca	ttc	cct	cag	gcc	355
Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	
70					75			80							85	
atc	gag	ggt	gat	gcg	ctt	ttt	gag	acg	ctt	gtc	gac	gcc	ccg	agc	cgc	403
Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	
				90				95						100		
ctg	cgg	ggt	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	
			105				110						115			
gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	
		120				125						130				
tta	gaa	ctc	ggg	gac	ccc	gtc	cat	tct	ctc	agt	gag	gaa	gat	ggg	gaa	547
Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	
135						140					145					
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	
150					155					160					165	
att	gcg	gtt	cca	ccg	gca	ctc	gct	gcc	gag	ttg	att	ggt	ttc	acc	cta	643
Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	
				170					175					180		
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	
			185				190						195			
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	
		200				205						210				
tcg	gct	ggg	ggt	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	
215						220					225					
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggt	gga	835
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	
230					235					240				245		
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	
				250				255						260		
gga	ttt	aat	cta	aaa	tct	taaacctcgt attttccctg ata										
Gly	Phe	Asn	Leu	Lys	Ser											
			265													

&lt;210&gt; 350

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly  
 1 5 10 15

Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn  
 20 25 30

Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser  
 35 40 45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp  
 50 55 60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly  
 65 70 75 80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val  
 85 90 95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly  
 100 105 110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln  
 115 120 125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser  
 130 135 140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg  
 145 150 155 160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu  
 165 170 175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His  
 180 185 190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu  
 195 200 205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln  
 210 215 220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala  
 225 230 235 240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln  
 245 250 255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser  
 260 265

&lt;210&gt; 351

&lt;211&gt; 636

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)

&lt;223&gt; RXA02159

&lt;400&gt; 351

tgatggacca gcgtccaaag ttttcgatga agcagaaaac cgcctccacg ctcagaaagc 60

actgctggtg tggctgctgg ccaaccagcc gaggtaagac atg tcc ctt ggc tca 115  
 Met Ser Leu Gly Ser  
 1 5

acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163  
 Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg  
 10 15 20

caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211  
 Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln  
 25 30 35

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259  
 Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln  
 40 45 50

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307  
 Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg  
 55 60 65

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355  
 Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile  
 70 75 80 85

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403  
 Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu  
 90 95 100

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451  
 Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu  
 105 110 115

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499  
 Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg  
 120 125 130

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547  
 Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val  
 135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595  
 Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu  
 150 155 160 165

ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct 636  
 Leu Ser Gly Arg Thr Thr  
 170

&lt;210&gt; 352

&lt;211&gt; 171

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 352

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val

290

295

300

Glu Thr Pro Glu His Ser Asn Thr Gln Pro  
305 310

&lt;210&gt; 347

&lt;211&gt; 1662

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1639)

&lt;223&gt; RXA01508

&lt;400&gt; 347

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ttccgggacg tttccgtgat ctcgtggaag atcccaaact ccgttccggt gccgtcgtgg 60
ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115
                                         Met Ser Asp Leu Gly
                                         1 5

ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala
                        10 15 20

tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu
                        25 30 35

aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val
                        40 45 50

gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp
                        55 60 65

cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly
                        70 75 80 85

ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln
                        90 95 100

tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val
                        105 110 115

ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu
                        120 125 130

gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala
                        135 140 145

gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

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1	5	10	15
Thr Arg Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln	20	25	30
Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly	35	40	45
Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly	50	55	60
Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly	65	70	75
Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys	85	90	95
Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly	100	105	110
Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala	115	120	125
Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala	130	135	140
Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys	145	150	155
Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr	165	170	

&lt;210&gt; 353

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(391)

&lt;223&gt; RXN02154

&lt;400&gt; 353

cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgccttg 60

caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115  
 Leu Lys Glu Gly Val  
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163  
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu  
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211  
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala  
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro  
90 95

ccttaaagcg gcg 414

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<210> 354
<211> 97
<212> PRT
<213> Corynebacterium glutamicum
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<400> 354
Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
  1                               5                                10                    15

Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
                20                              25                      30

Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
          35                        40                          45

Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
   50                            55                             60

Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
  65                               70                           75                   80

Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
              85                         90                     95
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Pro

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<210> 355
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (1279)  
<223> RXS00147
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<400> 355  
attgcatata atgcaatgaa ttgaataaac tacattcagg gttatcaacc agccaatttc 60

ttttaaaaag gcagacacac gaaaggcgac aacagtcacc gtg agt aaa gac acc 115  
Val Ser Lys Asp Thr  
1 5

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac	259
Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu  
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931  
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln  
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979  
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly  
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc  
 1027  
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc  
 1075  
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly  
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc  
 1123  
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca  
 1171  
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala  
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca  
 1219  
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag  
 1267  
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln  
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca  
 1302  
 Lys Lys Gly Ala  
 390

&lt;210&gt; 356

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser  
 1 5 10 15

Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe  
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr  
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95  
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
 290 295 300  
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala  
 385 390

<210> 357  
 <211> 924  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(901)  
 <223> RXS00905

<400> 357  
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tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115  
 Met Thr Gln Phe Glu  
 1 5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163  
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile  
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211  
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp  
 25 30 35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259  
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu  
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307  
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp  
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355  
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro  
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403  
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu  
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451  
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly  
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499  
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn  
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547  
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp  
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly  
 150 155 160 165  
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643  
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp  
 170 175 180  
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691  
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr  
 185 190 195  
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739  
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr  
 200 205 210  
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787  
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala  
 215 220 225  
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835  
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg  
 230 235 240 245  
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883  
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys  
 250 255 260  
 ctg gaa ggg cga gcc tta tgatccagag actttccgca ggc 924  
 Leu Glu Gly Arg Ala Leu  
 265

&lt;210&gt; 358

&lt;211&gt; 267

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn  
 1 5 10 15  
 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn  
 20 25 30  
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys  
 35 40 45  
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu  
 50 55 60  
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly  
 65 70 75 80  
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val  
 85 90 95  
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr  
 100 105 110  
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala  
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val  
 130 135 140  
 Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly  
 145 150 155 160  
 Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys  
 165 170 175  
 Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn  
 180 185 190  
 Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly  
 195 200 205  
 Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly  
 210 215 220  
 Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val  
 225 230 235 240  
 Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys  
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 Gln His His Arg Lys Leu Glu Gly Arg Ala Leu  
 260 265

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 <223> RXS00906

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 gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115  
 Met Asn Thr Asp Ala  
 1 5  
 ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163  
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro  
 10 15 20  
 tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211  
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val  
 25 30 35  
 gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259  
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg  
 40 45 50  
 cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307  
 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala  
 55 60 65

ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355  
 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val  
 70 75 80 85  
  
 cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403  
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His  
 90 95 100  
  
 ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451  
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp  
 105 110 115  
  
 gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499  
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser  
 120 125 130  
  
 acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547  
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val  
 135 140 145  
  
 acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595  
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu  
 150 155 160 165  
  
 gtc aac cca taagcagaat tggcactcta cgg 627  
 Val Asn Pro

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 <211> 168  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 360  
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 Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly  
 20 25 30  
  
 Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser  
 35 40 45  
  
 Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr  
 50 55 60  
  
 Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys  
 65 70 75 80  
  
 Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu  
 85 90 95  
  
 Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile  
 100 105 110  
  
 Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr  
 115 120 125  
  
 Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

130 135 140  
 Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys  
 145 150 155 160  
 Thr Glu Leu Ile Glu Val Asn Pro  
 165

<210> 361  
 <211> 246  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXS00907

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actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115  
 Leu Ala Leu Tyr Gly  
 1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163  
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp  
 10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211  
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu  
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aac tac acc aag tagacccaaa agcaggcggtt aac 246  
 Asn Tyr Thr Lys  
 40

<210> 362  
 <211> 41  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 362  
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Ala Leu Phe Leu Leu Asn Tyr Thr Lys  
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<220>

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 <222> (101)..(1258)  
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<400> 363

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gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115  
 Met Pro Val Ile Asn  
 1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163  
 Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu  
 10 15 20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211  
 His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe  
 25 30 35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259  
 Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly  
 40 45 50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307  
 Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly  
 55 60 65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355  
 Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu  
 70 75 80 85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403  
 Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala  
 90 95 100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451  
 Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr  
 105 110 115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499  
 Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln  
 120 125 130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547  
 Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly  
 135 140 145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595  
 Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln  
 150 155 160 165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643  
 Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met  
 170 175 180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691  
 Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His  
 185 190 195

ggc gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739  
 Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

200	205	210	
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val 215 220 225			787
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp 230 235 240 245			835
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe 250 255 260			883
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val 265 270 275			931
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn 280 285 290			979
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala 295 300 305			
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser 310 315 320 325			
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro 330 335 340			
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn 345 350 355			
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc 1219 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe 360 365 370			
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg 1268 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly 375 380 385			
cgctcgaaga tgc 1281			

&lt;210&gt; 364

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 364

Met Pro Val Ile Asn Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg  
 1 5 10 15

Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val  
 20 25 30

Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp  
 35 40 45

Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His  
 50 55 60

Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala  
 65 70 75 80

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro  
 85 90 95

Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu  
 100 105 110

Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val  
 115 120 125

Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val  
 130 135 140

Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr  
 145 150 155 160

Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr  
 165 170 175

Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr  
 180 185 190

Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile  
 195 200 205

Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg  
 210 215 220

Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His  
 225 230 235 240

Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala-Tyr Ile Asn Gly  
 245 250 255

Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg  
 260 265 270

Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala  
 275 280 285

Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala  
 290 295 300

Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val  
 305 310 315 320

Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe  
 325 330 335

Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser  
 340 345 350

Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro  
 355 360 365

Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu  
 370 375 380

Lys Gly  
 385

<210> 365  
 <211> 1386  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1363)  
 <223> RXS02101

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agtttttagtg tcgctgcgca ggtactctac tatctaatacc atg agc cgc att tca 115  
 Met Ser Arg Ile Ser  
 1 5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163  
 Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala  
 10 15 20

tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag 211  
 Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu  
 25 30 35

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259  
 Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val  
 40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307  
 Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly  
 55 60 65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355  
 Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp  
 70 75 80 85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403  
 Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg  
 90 95 100

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451  
 Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly  
 105 110 115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat	499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp	
120 125 130	
gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca	547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro	
135 140 145	
tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta	595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu	
150 155 160 165	
gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc	643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val	
170 175 180	
ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct	691
Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala	
185 190 195	
gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt	739
Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
200 205 210	
tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att	787
Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat	835
Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac	883
Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt	979
Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
280 285 290	
ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac	
1027 Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr	
295 300 305	
ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act	
1075 Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr	
310 315 320 325	
gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct	
1123 Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala	
330 335 340	
tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc	
1171	

Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe  
345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag  
1219

Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln  
360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc  
1267

Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala  
375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct  
1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala  
390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac  
1363

Ala Thr Arg Ala Ala Ala Ala Ala Leu Leu Thr Tyr Leu Gly Thr Asn  
410 415 420

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1386

<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser  
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Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg  
35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala  
50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met  
65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro  
85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val  
100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala  
115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile  
130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

145		150		155		160									
Val	Ala	Gly	Gly	Leu	Val	Asp	Leu	Ile	Pro	Arg	Pro	Asp	Val	Cys	Phe
				165					170					175	
Gly	Gln	His	Val	Val	Pro	Gly	Ala	Ala	Gly	Thr	Val	Met	Ser	Met	Pro
			180					185					190		
Gly	Gly	Ala	Leu	Ala	Ala	Cys	Asp	Ser	Ile	Glu	Ile	Arg	Ile	Gln	Gly
		195					200					205			
Arg	Ser	Ala	His	Gly	Ser	Met	Pro	His	Asn	Ser	Ile	Asp	Pro	Thr	Tyr
	210					215					220				
Val	Ala	Ala	Met	Ile	Val	Val	Arg	Leu	Gln	Gly	Ile	Val	Gly	Arg	Glu
225					230					235					240
Val	Ser	Pro	Glu	Asp	Phe	Ala	Val	Ile	Ser	Val	Gly	Thr	Leu	Gln	Ser
				245					250					255	
Gly	Asn	Thr	Asn	Asn	Thr	Ile	Pro	Ala	Ser	Ala	Arg	Leu	Val	Leu	Asn
			260					265					270		
Cys	Arg	Phe	Tyr	Asn	Asp	Lys	Val	Lys	His	Lys	Val	Tyr	Arg	Ala	Ile
		275					280					285			
Glu	Arg	Val	Val	Arg	Gly	Glu	Cys	Leu	Ala	Ser	Gly	Ile	Glu	Glu	Glu
	290					295					300				
Pro	Val	Ile	Glu	Tyr	Phe	Ala	His	Gly	Asp	Leu	Thr	Asn	Asn	Thr	Pro
305					310					315					320
Val	Val	Phe	Asp	Thr	Val	Arg	Pro	Val	Phe	Asp	Asp	Val	Phe	Gly	Glu
				325					330					335	
Asp	Ser	Ile	Asp	Ala	Tyr	Arg	Trp	Thr	Ala	Ser	Glu	Asp	Phe	Pro	Ser
			340					345					350		
Ile	Pro	Lys	Ala	Phe	Asn	Ser	Pro	Tyr	Leu	Tyr	Trp	Thr	Ile	Gly	Val
		355					360					365			
Thr	Pro	Arg	Asp	Gln	Trp	Thr	Glu	Ala	Val	Glu	Arg	Asp	Arg	Val	Ala
	370					375					380				
Ser	Asp	Val	Pro	Ala	Asn	His	Met	Gly	Asp	Phe	Leu	Pro	Asp	Tyr	Ala
385					390					395					400
Pro	Thr	Met	Ser	Ala	Ala	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Thr
				405				410						415	
Tyr	Leu	Gly	Thr	Asn											
			420												

&lt;210&gt; 367

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (3439)

&lt;223&gt; RXS02234

&lt;400&gt; 367

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tgatggatgc agacgctcag aagaaaggcg cataaataac	atg cca aag cgt tca	115
	Met Pro Lys Arg Ser	
	1 5	

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc	163
Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly	
10 15 20	

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg	211
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu	
25 30 35	

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg	259
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr	
40 45 50	

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc	307
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile	
55 60 65	

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc	355
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly	
70 75 80 85	

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt	403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu	
90 95 100	

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc	451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly	
105 110 115	

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat	499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp	
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cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg	547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala	
135 140 145	

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca	595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala	
150 155 160 165	

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Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly	
170 175 180	

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct	691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala	
185 190 195	

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa	739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu	
200 205 210	

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Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr	
215 220 225	
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Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu	
230 235 240 245	
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg	883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu	
250 255 260	
act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc	931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
265 270 275	
cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc	979
Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile	
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1171	
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1267	
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1363	
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410 415 420	

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cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt  
 1459  
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu  
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 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp  
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 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val  
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 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met  
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 1699  
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val  
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 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val  
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aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca  
 1891  
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala  
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 1939  
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys  
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aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac  
 1987  
 Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr  
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ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag  
 2035  
 Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu  
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 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val  
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 2179  
 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu  
 680 685 690

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 2275  
 Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser  
 710 715 720 725

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 Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met  
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 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp  
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 Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn  
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 Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr  
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 Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys  
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Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly	85	90	95	
Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile	100	105	110	
Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile	115	120	125	
Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile	130	135	140	
Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val	145	150	155	160
His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser	165	170	175	
Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	180	185	190	
Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	195	200	205	
Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	Glu	210	215	220	
Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	Glu	225	230	235	240
Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala	245	250	255	
Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	Gln	260	265	270	
Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn	275	280	285	
Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	Glu	290	295	300	
Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr	305	310	315	320
Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr	325	330	335	
Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe	340	345	350	
Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe	355	360	365	
Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser	370	375	380	
Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn	385	390	395	400

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 420 425 430  
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 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe  
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 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg  
 485 490 495  
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg  
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 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu  
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 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe  
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 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala  
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 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile  
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 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
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 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
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 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
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 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val  
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Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met	Thr
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Lys	Asp	Asp	Ile	Leu	Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser	Arg
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Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu
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Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg
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Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val
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Ile	Arg	Glu	Gly	Glu	Val	Asp	Leu	Ile	Leu	Asn	Thr	Pro	Ala	Gly	Ser
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Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val  
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 Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
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Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly	
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gtt	ggc	tat	ggc	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa	
1267																
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu	
	375					380					385					

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat  
 1315  
 Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp  
 390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta  
 1363  
 Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu  
 410 415 420

ggc taaaaacatg aagcaggagt ctt  
 1389  
 Gly

<210> 372  
 <211> 422  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 372  
 Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu  
 1 5 10 15  
 Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys  
 20 25 30  
 Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly  
 35 40 45  
 Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val  
 50 55 60  
 Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu  
 65 70 75 80  
 Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe  
 85 90 95  
 Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly  
 100 105 110  
 Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala  
 115 120 125  
 Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu  
 130 135 140  
 Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro  
 145 150 155 160  
 Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly  
 165 170 175  
 Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser  
 180 185 190  
 Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala  
 195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp  
 210 215 220  
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala  
 225 230 235 240  
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu  
 245 250 255  
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val  
 260 265 270  
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu  
 275 280 285  
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp  
 290 295 300  
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile  
 305 310 315 320  
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg  
 325 330 335  
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala  
 340 345 350  
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly  
 355 360 365  
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu  
 370 375 380  
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala  
 385 390 395 400  
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val  
 405 410 415  
 Val Arg Glu Phe Leu Gly  
 420

<210> 373  
 <211> 525  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(502)  
 <223> RXS02937

<400> 373  
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 tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115  
 Val Ile Ser Asn Gly  
 1 5  
 gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

Glu	Gly	Pro	Val	Val	Ala	Leu	Arg	Gly	Asp	Ile	Asp	Ala	Leu	Pro	Met	
				10					15					20		
gcg	gag	cga	tcc	ggc	aaa	gaa	tac	gca	gca	acc	gga	gtg	aca	cag	gtg	211
Ala	Glu	Arg	Ser	Gly	Lys	Glu	Tyr	Ala	Ala	Thr	Gly	Val	Thr	Gln	Val	
			25					30					35			
gat	aac	acc	acc	ggt	caa	gaa	act	ccg	gtg	gcg	cat	acc	tgt	ggc	cac	259
Asp	Asn	Thr	Thr	Gly	Gln	Glu	Thr	Pro	Val	Ala	His	Thr	Cys	Gly	His	
		40					45					50				
gat	gtg	cat	att	tca	tca	ctg	ttg	ggt	gcg	gtg	cag	gcg	ttc	aat	tct	307
Asp	Val	His	Ile	Ser	Ser	Leu	Leu	Gly	Ala	Val	Gln	Ala	Phe	Asn	Ser	
	55					60					65					
cat	cgg	gaa	ttg	tgg	aac	gga	acg	ttg	atg	gcc	gtt	ttc	cag	cca	gcg	355
His	Arg	Glu	Leu	Trp	Asn	Gly	Thr	Leu	Met	Ala	Val	Phe	Gln	Pro	Ala	
	70				75					80					85	
gaa	gag	acg	gca	gct	ggt	gcg	agg	atg	atg	gcg	gat	cag	gac	aac	gcg	403
Glu	Glu	Thr	Ala	Ala	Gly	Ala	Arg	Met	Met	Ala	Asp	Gln	Asp	Asn	Ala	
				90					95					100		
ccg	gga	aat	cac	tct	cca	gcg	ttc	gcg	cca	gat	atg	cag	cca	act	ctt	451
Pro	Gly	Asn	His	Ser	Pro	Ala	Phe	Ala	Pro	Asp	Met	Gln	Pro	Thr	Leu	
			105					110					115			
gat	cgt	ggt	gtg	gaa	gcg	ctg	gtt	gta	gct	gct	tct	gcg	tgg	cta	gta	499
Asp	Arg	Gly	Val	Glu	Ala	Leu	Val	Val	Ala	Ala	Ser	Ala	Trp	Leu	Val	
		120					125					130				
aaa	taattggcta	atgaatcctt	ttc													525
Lys																

&lt;210&gt; 374

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 374

Val	Ile	Ser	Asn	Gly	Glu	Gly	Pro	Val	Val	Ala	Leu	Arg	Gly	Asp	Ile	
1				5					10					15		
Asp	Ala	Leu	Pro	Met	Ala	Glu	Arg	Ser	Gly	Lys	Glu	Tyr	Ala	Ala	Thr	
			20					25					30			
Gly	Val	Thr	Gln	Val	Asp	Asn	Thr	Thr	Gly	Gln	Glu	Thr	Pro	Val	Ala	
		35					40					45				
His	Thr	Cys	Gly	His	Asp	Val	His	Ile	Ser	Ser	Leu	Leu	Gly	Ala	Val	
	50					55					60					
Gln	Ala	Phe	Asn	Ser	His	Arg	Glu	Leu	Trp	Asn	Gly	Thr	Leu	Met	Ala	
	65				70					75					80	
Val	Phe	Gln	Pro	Ala	Glu	Glu	Thr	Ala	Ala	Gly	Ala	Arg	Met	Met	Ala	
				85					90					95		
Asp	Gln	Asp	Asn	Ala	Pro	Gly	Asn	His	Ser	Pro	Ala	Phe	Ala	Pro	Asp	

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<210> 375
<211> 966
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(943)  
<223> RXA02194
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gaaatctccc agctcattta ttggacccag gtcatcatgg ttgctcgcgg cctgaagcca 60															
gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115															
Met Leu Lys Ile Ala 5															
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163															
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala 20															
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211															
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe 35															
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259															
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile 50															
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307															
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg 65															
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355															
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu 85															
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403															
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu 100															
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451															
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro 115															
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499															
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val 130															
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547															
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala 145															

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595  
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln  
150 155 160 165

ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643  
Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile  
170 175 180

gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691  
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu  
185 190 195

cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739  
Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp  
200 205 210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787  
Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro  
215 220 225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835  
Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val  
230 235 240 245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883  
Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp  
250 255 260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931  
Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg  
265 270 275

atc gcc cgc atc tagttttaac taccctcgaa aat 966  
Ile Ala Arg Ile  
280

&lt;210&gt; 376

&lt;211&gt; 281

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala  
1 5 10 15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys  
20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu  
35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu  
50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His  
65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala  
85 90 95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile  
 100 105 110  
 Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly  
 115 120 125  
 Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile  
 130 135 140  
 Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg  
 145 150 155 160  
 Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr  
 165 170 175  
 Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu  
 180 185 190  
 Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn  
 195 200 205  
 Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala  
 210 215 220  
 Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala  
 225 230 235 240  
 Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala  
 245 250 255  
 Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu  
 260 265 270  
 Ala Ser Glu Ile Arg Ile Ala Arg Ile  
 275 280

<210> 377  
 <211> 393  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (370)  
 <223> RXA02195

<400> 377  
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 tcctccccca aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115  
 Met Tyr Arg Val Lys  
 1 5  
 aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163  
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg  
 10 15 20  
 cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211  
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

25					30					35						
cta	ggt	aag	aag	gtc	atc	gaa	gaa	gcc	gga	gag	gtc	tgg	att	gca	gcc	259
Leu	Gly	Lys	Lys	Val	Ile	Glu	Glu	Ala	Gly	Glu	Val	Trp	Ile	Ala	Ala	
		40					45					50				
gag	tat	gag	acc	gat	gaa	gag	cta	gcc	gga	gaa	atc	tcc	cag	ctc	att	307
Glu	Tyr	Glu	Thr	Asp	Glu	Glu	Leu	Ala	Gly	Glu	Ile	Ser	Gln	Leu	Ile	
		55					60					65				
tat	tgg	acc	cag	gtc	atc	atg	gtt	gct	cgc	ggc	ctg	aag	cca	gaa	gat	355
Tyr	Trp	Thr	Gln	Val	Ile	Met	Val	Ala	Arg	Gly	Leu	Lys	Pro	Glu	Asp	
		70					75					80			85	
atc	tac	aag	aac	ctg	taggagtttt	aaagcaatca	tgt									393
Ile	Tyr	Lys	Asn	Leu												
				90												

<210> 378  
 <211> 90  
 <212> PRT  
 <213> Corynebacterium glutamicum

Met	Tyr	Arg	Val	Lys	Thr	Phe	Asp	Ser	Leu	Tyr	Glu	Glu	Leu	Leu	Asn
1				5					10					15	
Arg	Ala	Gln	Thr	Arg	Pro	Glu	Gly	Ser	Gly	Thr	Val	Ala	Ala	Leu	Asp
			20					25					30		
Lys	Gly	Ile	His	His	Leu	Gly	Lys	Lys	Val	Ile	Glu	Glu	Ala	Gly	Glu
		35					40					45			
Val	Trp	Ile	Ala	Ala	Glu	Tyr	Glu	Thr	Asp	Glu	Glu	Leu	Ala	Gly	Glu
		50				55					60				
Ile	Ser	Gln	Leu	Ile	Tyr	Trp	Thr	Gln	Val	Ile	Met	Val	Ala	Arg	Gly
		65			70					75					80
Leu	Lys	Pro	Glu	Asp	Ile	Tyr	Lys	Asn	Leu						
				85					90						

<210> 379  
 <211> 477  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(454)  
 <223> RXA01097

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taaagggagc	cattaaagat	gcaggatttg	aggtgcggaa	atg	agt	gac	aat
				Met	Ser	Asp	Asn
				1			5
							115

caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163  
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn  
                     10                    15                    20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211  
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu  
                     25                    30                    35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259  
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu  
                     40                    45                    50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307  
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp  
                     55                    60                    65

atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355  
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala  
                     70                    75                    80                    85

ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403  
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly  
                     90                    95                    100

ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451  
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu  
                     105                    110                    115

ctg taaaagcaac aacgattaag gaa 477  
 Leu

&lt;210&gt; 380

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys  
           1                    5                    10                    15

Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala  
                     20                    25                    30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala  
                     35                    40                    45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser  
                     50                    55                    60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu  
                     65                    70                    75                    80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr  
                     85                    90                    95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe  
                     100                    105                    110

Asp Asn Asp Val Leu Leu

<210> 381  
<211> 861  
<212> DNA  
<213> *Corynebacterium glutamicum*

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<220>  
<221> CDS  
<222> (101)..(838)  
<223> RXA01100
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aaactggatc aactacatct aacagatagg atcaatattc atg acc ttc act att 115  
Met Thr Phe Thr Ile  
1 5

ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag 163  
 Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln  
 10 15 20

ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca 211  
Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala  
25 30 35

ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg 259  
Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu  
40 .45 50

gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att 307  
Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile  
55 60 65

gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat 355  
Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp  
70 75 80 85

gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac 403  
Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn  
90 95 100

att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att 451  
Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile  
105 110 115

caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa 499  
Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu  
120 125 130

gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc 547  
Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly  
135 140 145

gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt 595  
Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg  
150 155 160 165

ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat 643

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn  
 170 175 180  
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691  
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val  
 185 190 195  
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739  
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys  
 200 205 210  
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787  
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr  
 215 220 225  
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835  
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu  
 230 235 240 245  
 ggt taatacatgg atgctcgtgg gat 861  
 Gly

<210> 382  
 <211> 246  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala  
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 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr  
 20 25 30  
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu  
 35 40 45  
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu  
 50 55 60  
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr  
 65 70 75 80  
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly  
 85 90 95  
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp  
 100 105 110  
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile  
 115 120 125  
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp  
 130 135 140  
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser  
 145 150 155 160  
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

				165					170					175	
Leu	Ser	Gly	Pro	Asn	Val	Glu	Leu	Leu	Arg	Glu	Val	Ala	Ala	Ala	Thr
			180					185					190		
Asp	Ala	Pro	Ile	Val	Ala	Ser	Gly	Gly	Ile	Ser	Val	Leu	Glu	Asp	Val
		195					200					205			
Leu	Glu	Leu	Ala	Lys	Tyr	Gln	Asp	Glu	Gly	Ile	Asp	Ser	Val	Ile	Ile
	210					215					220				
Gly	Lys	Ala	Leu	Tyr	Glu	His	Lys	Phe	Thr	Leu	Glu	Glu	Ala	Leu	Ala
225					230					235					240
Ala	Val	Glu	Lys	Leu	Gly										
				245											

&lt;210&gt; 383

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(733)

&lt;223&gt; RXA01101

&lt;400&gt; 383

atcgcagcta ggccagtgtg gtggatataa aacccttttg gggagaaaga aactcgactg 60

cggttcttga	tcctgaaagc	acgtgacata	aactatcggc	atg	acc	aaa	act	gtc	115
				Met	Thr	Lys	Thr	Val	
				1				5	

gcc	ctt	ctc	gac	tac	gga	tct	gga	aac	ctt	cgt	tct	gct	caa	cgc	gca	163
Ala	Leu	Leu	Asp	Tyr	Gly	Ser	Gly	Asn	Leu	Arg	Ser	Ala	Gln	Arg	Ala	
				10				15						20		

cta	gag	cgt	gcc	ggt	gca	gaa	gtt	atc	gtg	agc	tcc	gat	cca	gaa	gtt	211
Leu	Glu	Arg	Ala	Gly	Ala	Glu	Val	Ile	Val	Ser	Ser	Asp	Pro	Glu	Val	
			25				30						35			

tgc	acc	aac	gct	gat	ggc	ctc	cta	gtt	cct	gga	gtg	ggc	gca	ttt	gat	259
Cys	Thr	Asn	Ala	Asp	Gly	Leu	Leu	Val	Pro	Gly	Val	Gly	Ala	Phe	Asp	
		40				45						50				

gcc	tgc	atg	aag	ggt	ttg	aaa	aac	gtc	ttc	gga	cat	cgc	att	atc	gga	307
Ala	Cys	Met	Lys	Gly	Leu	Lys	Asn	Val	Phe	Gly	His	Arg	Ile	Ile	Gly	
	55					60					65					

cag	cgt	ctt	gct	ggt	gga	cgt	cca	gtg	atg	ggt	att	tgt	gtg	ggc	atg	355
Gln	Arg	Leu	Ala	Gly	Gly	Arg	Pro	Val	Met	Gly	Ile	Cys	Val	Gly	Met	
	70				75					80					85	

cag	atc	ctg	ttc	gat	gaa	ggc	gat	gag	cac	ggc	att	aag	tca	gct	ggt	403
Gln	Ile	Leu	Phe	Asp	Glu	Gly	Asp	Glu	His	Gly	Ile	Lys	Ser	Ala	Gly	
				90					95					100		

tgc	ggc	gag	tgg	cct	ggc	aaa	gtg	gaa	cgc	ctc	caa	gcg	gag	atc	ctg	451
Cys	Gly	Glu	Trp	Pro	Gly	Lys	Val	Glu	Arg	Leu	Gln	Ala	Glu	Ile	Leu	

105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met 120 125 130			499
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr 135 140 145			547
ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro 150 155 160 165			595
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val 170 175 180			643
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly 185 190 195			691
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile 200 205 210			733
taacagatag gatcaatatt cat			756

&lt;210&gt; 384

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg 1 5 10 15
Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser 20 25 30
Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly 35 40 45
Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly 50 55 60
His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly 65 70 75 80
Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly 85 90 95
Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu 100 105 110
Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro 115 120 125
Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr 130 135 140

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp  
145 150 155 160

Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg  
165 170 175

Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His  
180 185 190

Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile  
195 200 205

Asn Tyr Ile  
210

<210> 385

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01657

<400> 385

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cgcacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
Val Ile Val Gly Val  
1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130  
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547  
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145  
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165  
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643  
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp  
 170 175 180  
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691  
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu  
 185 190 195  
 ctg gcg att tgatgttttc ggtagcgctc tgt 723  
 Leu Ala Ile  
 200

&lt;210&gt; 386

&lt;211&gt; 200

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 386

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15  
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30  
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45  
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60  
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80  
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95  
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110  
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125  
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140  
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro  
 165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val  
 180 185 190

Arg Lys His Ala Glu Leu Ala Ile  
 195 200

<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

cctccgtcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
 Val Ile Val Gly Val  
 1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165

caa ggc 601  
 Gln Gly

<210> 388  
 <211> 167  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 388  
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val Val Gly Val Arg Gln Gly  
 165

<210> 389  
 <211> 897  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(874)  
 <223> RXA01098

&lt;400&gt; 389

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aaaagggctc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60

gcaggtaatg accagtcgtt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                   Met Gly Val Ala Ile
                                   1                               5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
                        10                               15                               20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
                        25                               30                               35

aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
                        40                               45                               50

acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
                        55                               60                               65

acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
                        70                               75                               80                               85

agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
                        90                               95                               100

tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
                        105                               110                               115

tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
                        120                               125                               130

cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
                        135                               140                               145

acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
                        150                               155                               160                               165

aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
                        170                               175                               180

gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
                        185                               190                               195

gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
                        200                               205                               210

aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

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Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val  
 215 220 225  
 ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835  
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val  
 230 235 240 245  
 aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884  
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys  
 250 255  
 tccacaagag tat 897

<210> 390  
 <211> 258  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 390

Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly  
 1 5 10 15  
 Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp  
 20 25 30  
 Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu  
 35 40 45  
 Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu  
 50 55 60  
 Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80  
 Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala  
 85 90 95  
 Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu  
 100 105 110  
 Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu  
 115 120 125  
 Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser  
 130 135 140  
 Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp  
 145 150 155 160  
 Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile  
 165 170 175  
 Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu  
 180 185 190  
 Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala  
 195 200 205  
 Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala  
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val  
225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val  
245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115  
Met Thr Val Ala Pro  
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
120 125 130

ggg gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
 135 140 145  
 gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
 150 155 160 165  
 gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
 170 175 180  
 ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
 185 190 195  
 act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
 200

<210> 392  
 <211> 202  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 392  
 Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
 1 5 10 15  
 Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
 20 25 30  
 Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
 35 40 45  
 Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
 50 55 60  
 Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
 65 70 75 80  
 Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
 85 90 95  
 Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
 100 105 110  
 Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
 115 120 125  
 Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
 130 135 140  
 Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
 145 150 155 160  
 Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
 165 170 175  
 Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
 195 200

<210> 393  
 <211> 729  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(706)  
 <223> FRXA01104

<400> 393  
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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115  
 Met Thr Val Ala Pro  
 1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
 10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
 25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
 40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
 55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
 70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
 90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
 105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
 120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547  
 Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
 135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
 150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
                   170                  175                  180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
                   185                  190                  195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
                   200

<210> 394

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
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Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
                   20                  25                  30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
                   35                  40                  45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
   50                  55                  60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
   65                  70                  75                  80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
                   85                  90                  95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
                   100                  105                  110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
                   115                  120                  125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
   130                  135                  140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
   145                  150                  155                  160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
                   165                  170                  175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
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Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
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 <223> RXN00446

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 Met Gly Ala Val Glu  
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ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc 163  
 Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val  
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acg gta ggt tgc ggc tcg tct gcg ctg tgt caa cag ctg gtt cag gca 211  
 Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala  
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acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag 259  
 Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu  
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gct tat cca att ttc gcg cag gtc gcg ggc gcc act cct gtt gcc att 307  
 Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile  
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ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg 355  
 Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala  
 70 75 80 85

atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct 403  
 Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro  
 90 95 100

tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag 451  
 Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys  
 105 110 115

gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc 499  
 Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe  
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aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac 547  
 Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His  
 135 140 145

gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg 595  
 Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala  
 150 155 160 165

ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg 643  
 Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala  
 170 175 180

atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg 691

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala  
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739  
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val  
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787  
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala  
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835  
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala  
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 280 285

tgc 987

&lt;210&gt; 396

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val  
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Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130	135	140
Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys 145 150 155 160		
Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala 165 170 175		
Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn 180 185 190		
Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu 195 200 205		
Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val 210 215 220		
Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro 225 230 235 240		
Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile 245 250 255		
Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala 260 265 270		
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cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr 35 40 45	144
ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile 50 55 60	192
atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca	240

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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
65                               70                               75                               80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg      288
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
                               85                               90                               95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg      336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
                               100                              105                              110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag      384
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
                               115                              120                              125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att      432
Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
                               130                              135                              140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa      480
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
145                               150                              155                              160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg      522
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
                               165                              170

tagtctttgg cgttttgcgg tgc      545

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&lt;210&gt; 398

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398

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Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
1                               5                               10                               15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
                               20                               25                               30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
                               35                               40                               45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
                               50                               55                               60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
65                               70                               75                               80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
                               85                               90                               95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
100                              105                              110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
115                              120                              125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

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130	135	140	
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Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly			
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 Met Thr Lys Ile Thr 5  
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ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163  
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr 20  
 10 15

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211  
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn 35  
 25 30

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259  
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val 50  
 40 45

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307  
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val 65  
 55 60

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355  
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val 85  
 70 75 80

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403  
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile 100  
 90 95

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451  
 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu 115  
 105 110

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499  
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr 130  
 120 125

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547  
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp 145  
 135 140

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Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val	
150 155 160 165	
ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac	643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp	
170 175 180	
gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027	
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075	
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123	
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
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cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171	
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
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360 365	

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			20					25					30		
Asn	Thr	Asn	Glu	Asn	Pro	Tyr	Pro	Pro	Ser	Glu	Ala	Leu	Val	Ala	Asp
		35					40					45			
Leu	Val	Ala	Thr	Val	Asp	Lys	Ile	Ala	Thr	Glu	Leu	Asn	Arg	Tyr	Pro
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Glu	Arg	Asp	Ala	Val	Glu	Leu	Arg	Asp	Glu	Leu	Ala	Ala	Tyr	Ile	Thr
65					70					75					80
Lys	Gln	Thr	Gly	Val	Ala	Val	Thr	Arg	Asp	Asn	Leu	Trp	Ala	Ala	Asn
				85					90					95	
Gly	Ser	Asn	Glu	Ile	Leu	Gln	Gln	Leu	Leu	Gln	Ala	Phe	Gly	Gly	Pro
			100					105					110		
Gly	Arg	Thr	Ala	Leu	Gly	Phe	Gln	Pro	Ser	Tyr	Ser	Met	His	Pro	Ile
		115					120					125			
Leu	Ala	Lys	Gly	Thr	His	Thr	Glu	Phe	Ile	Ala	Val	Ser	Arg	Gly	Ala
	130					135					140				
Asp	Phe	Arg	Ile	Asp	Met	Asp	Val	Ala	Leu	Glu	Glu	Ile	Arg	Ala	Lys
145					150					155					160
Gln	Pro	Asp	Ile	Val	Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp
				165					170					175	
Val	Thr	Ser	Leu	Asp	Asp	Val	Glu	Arg	Ile	Ile	Asn	Val	Ala	Pro	Gly
			180					185					190		
Ile	Val	Ile	Val	Asp	Glu	Ala	Tyr	Ala	Glu	Phe	Ser	Pro	Ser	Pro	Ser
		195					200					205			
Ala	Thr	Thr	Leu	Leu	Glu	Lys	Tyr	Pro	Thr	Lys	Leu	Val	Val	Ser	Arg
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Thr	Met	Ser	Lys	Ala	Phe	Asp	Phe	Ala	Gly	Gly	Arg	Leu	Gly	Tyr	Phe
225					230					235					240
Val	Ala	Asn	Pro	Ala	Phe	Ile	Asp	Ala	Val	Met	Leu	Val	Arg	Leu	Pro
				245					250					255	
Tyr	His	Leu	Ser	Ala	Leu	Ser	Gln	Ala	Ala	Ala	Ile	Val	Ala	Leu	Arg
			260				265						270		

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg  
 275 280 285  
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro  
 290 295 300  
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala  
 305 310 315 320  
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335  
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 340 345 350  
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
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 Met Leu Asn Val Thr  
 1 5  
 gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163  
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu  
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 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro  
 25 30 35  
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 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr  
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 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala  
 55 60 65  
 gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355  
 Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu  
 70 75 80 85  
 tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403  
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln  
 90 95 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	
1027	
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	
1075	
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	
1123	
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340  
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc  
 1171  
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly  
 345 350 355  
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac  
 1219  
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His  
 360 365 370  
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg  
 1267  
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr  
 375 380 385  
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct  
 1315  
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala  
 390 395 400 405  
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat  
 1363  
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp  
 410 415 420  
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 1411  
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro  
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 Thr Thr Asp Glu Ala  
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 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu  
 20 25 30  
 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu  
 35 40 45  
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser  
 50 55 60  
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp  
 65 70 75 80  
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys  
 85 90 95

Val	His	Ala	Glu	Gln	Lys	Pro	Ser	Glu	His	Thr	Thr	Glu	Leu	Ser	Pro	100	105	110
Gly	Gly	Thr	Val	Thr	Glu	Arg	Phe	Met	Pro	Ile	Asp	Arg	Val	Gly	Leu	115	120	125
Tyr	Val	Pro	Gly	Gly	Asn	Ala	Val	Tyr	Pro	Ser	Ser	Val	Ile	Met	Asn	130	135	140
Thr	Val	Pro	Ala	Gln	Glu	Ala	Gly	Val	Asn	Ser	Leu	Val	Val	Ala	Ser	145	150	155
Pro	Pro	Gln	Ala	Glu	His	Gly	Gly	Trp	Pro	His	Pro	Thr	Ile	Leu	Ala	165	170	175
Ala	Cys	Ser	Ile	Leu	Gly	Val	Asp	Glu	Val	Trp	Ala	Val	Gly	Gly	Gly	180	185	190
Gln	Ala	Val	Ala	Leu	Leu	Ala	Tyr	Gly	Asp	Asp	Ala	Ala	Gly	Leu	Glu	195	200	205
Pro	Val	Asp	Met	Ile	Thr	Gly	Pro	Gly	Asn	Ile	Phe	Val	Thr	Ala	Ala	210	215	220
Lys	Arg	Leu	Val	Arg	Gly	Val	Val	Gly	Thr	Asp	Ser	Glu	Ala	Gly	Pro	225	230	235
Thr	Glu	Ile	Ala	Val	Leu	Ala	Asp	Ala	Ser	Ala	Asn	Ala	Val	Asn	Val	245	250	255
Ala	Tyr	Asp	Leu	Ile	Ser	Gln	Ala	Glu	His	Asp	Val	Met	Ala	Ala	Ser	260	265	270
Val	Leu	Ile	Thr	Asp	Ser	Glu	Gln	Leu	Ala	Lys	Asp	Val	Asn	Arg	Glu	275	280	285
Ile	Glu	Ala	Arg	Tyr	Ser	Ile	Thr	Arg	Asn	Ala	Glu	Arg	Val	Ala	Glu	290	295	300
Ala	Leu	Arg	Gly	Ala	Gln	Ser	Gly	Ile	Val	Leu	Val	Asp	Asp	Ile	Ser	305	310	315
Val	Gly	Ile	Gln	Val	Ala	Asp	Gln	Tyr	Ala	Ala	Glu	His	Leu	Glu	Ile	325	330	335
His	Thr	Glu	Asn	Ala	Arg	Ala	Val	Ala	Glu	Gln	Ile	Thr	Asn	Ala	Gly	340	345	350
Ala	Ile	Phe	Val	Gly	Asp	Phe	Ser	Pro	Val	Pro	Leu	Gly	Asp	Tyr	Ser	355	360	365
Ala	Gly	Ser	Asn	His	Val	Leu	Pro	Thr	Ser	Gly	Ser	Ala	Arg	Phe	Ser	370	375	380
Ala	Gly	Leu	Ser	Thr	His	Thr	Phe	Leu	Arg	Pro	Val	Asn	Leu	Ile	Glu	385	390	395
Tyr	Asp	Glu	Ala	Ala	Leu	Lys	Asp	Val	Ser	Gln	Val	Val	Ile	Asn	Phe	405	410	415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg  
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Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala  
 435 440

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 <213> Corynebacterium glutamicum

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 <223> RXC00930

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 ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115  
 Met Ser Gly His Ser  
 1 5  
 aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163  
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg  
 10 15 20  
 ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211  
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg  
 25 30 35  
 aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259  
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile  
 40 45 50  
 aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307  
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala  
 55 60 65  
 cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355  
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn  
 70 75 80 85  
 atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403  
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu  
 90 95 100  
 tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451  
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala  
 105 110 115  
 atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499  
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr  
 120 125 130  
 atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547  
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser  
 135 140 145  
 gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val  
 150 155 160 165  
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643  
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile  
 170 175 180  
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691  
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp  
 185 190 195  
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739  
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp  
 200 205 210  
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787  
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp  
 215 220 225  
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835  
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu  
 230 235 240 245  
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 Thr Glu Leu Glu Asn Asp  
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 <213> Corynebacterium glutamicum

<400> 404  
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 35 40 45  
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp  
 50 55 60  
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly  
 65 70 75 80  
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val  
 85 90 95  
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr  
 100 105 110  
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser  
 115 120 125  
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln  
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala  
 145 150 155 160  
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys  
 165 170 175  
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly  
 180 185 190  
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val  
 195 200 205  
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala  
 210 215 220  
 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu  
 225 230 235 240  
 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp  
 245 250

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXC01096

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 Met Lys Pro Arg Val  
 1 5  
 ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163  
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser  
 10 15 20  
 tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211  
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly  
 25 30 35  
 agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259  
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met  
 40 45 50  
 gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307  
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu  
 55 60 65  
 aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355  
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala  
 70 75 80 85  
 gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403  
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

90										95					100					
gca	gaa	cgg	gcc	cga	acc	ctg	ctg	acc	tcc	ggt	gtg	gcc	tca	cag	aag	451				
Ala	Glu	Arg	Ala	Arg	Thr	Leu	Leu	Thr	Ser	Gly	Val	Ala	Ser	Gln	Lys					
			105					110					115							
gct	aat	tcc	gga	acc	ctg	ctg	tct	gat	tgg	gcg	gag	atc	atc	aat	acc	499				
Ala	Asn	Ser	Gly	Thr	Leu	Leu	Ser	Asp	Trp	Ala	Glu	Ile	Ile	Asn	Thr					
		120					125					130								
acc	acc	cat	cca	ctg	gcg	gca	gtg	gta	gcc	atg	att	ggc	tgc	gcg	cta	547				
Thr	Thr	His	Pro	Leu	Ala	Ala	Val	Val	Ala	Met	Ile	Gly	Cys	Ala	Leu					
		135				140					145									

&lt;210&gt; 406

&lt;211&gt; 149

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 406

Met	Lys	Pro	Arg	Val	Leu	Ser	Ala	Leu	Gly	Ile	Gly	Ala	Gly	Ala	Leu
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Val	Val	Trp	Ile	Ser	Ser	Arg	Met	Asn	Trp	Val	Thr	Ile	Glu	Ala	Phe
			20					25					30		
Asp	Asp	Lys	Ser	Gly	Ser	Val	Thr	Gln	Ser	Ile	Val	Gly	Ala	Thr	Trp
		35					40					45			
Ser	Thr	Glu	Ile	Met	Ala	Leu	Ala	Leu	Ala	Leu	Leu	Ala	Ala	Phe	Ala
	50					55					60				
Ala	Ala	Leu	Val	Leu	Lys	Arg	Met	Gly	Arg	Arg	Ile	Ile	Gly	Gly	Ile
65					70				75						80
Ser	Ala	Leu	Ile	Ala	Val	Gly	Ala	Ser	Leu	Ser	Pro	Leu	Ala	Leu	Leu
				85					90					95	
Thr	Gln	Asp	Pro	Asp	Ala	Glu	Arg	Ala	Arg	Thr	Leu	Leu	Thr	Ser	Gly
			100					105					110		
Val	Ala	Ser	Gln	Lys	Ala	Asn	Ser	Gly	Thr	Leu	Leu	Ser	Asp	Trp	Ala
		115					120					125			
Glu	Ile	Ile	Asn	Thr	Thr	Thr	His	Pro	Leu	Ala	Ala	Val	Val	Ala	Met
	130					135					140				
Ile	Gly	Cys	Ala	Leu											
145															

&lt;210&gt; 407

&lt;211&gt; 1020

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (997)

&lt;223&gt; RXC01656

&lt;400&gt; 407

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atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115  
Met Thr Glu Thr Gln  
1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163  
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met  
10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211  
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg  
25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259  
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val  
40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307  
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro  
55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355  
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala  
70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403  
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu  
90 95 100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451  
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr  
105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499  
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly  
120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547  
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala  
135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595  
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala  
150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643  
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser  
170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691  
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro  
185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739  
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val  
200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val  
 215 220 225  
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835  
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys 245  
 230 235 240  
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883  
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr 260  
 250 255  
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931  
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly 275  
 265 270  
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979  
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg 290  
 280 285  
 ctc gcc gag cgc ggc tgg tgatcggttg agtttttagct ctc  
 1020  
 Leu Ala Glu Arg Gly Trp  
 295

&lt;210&gt; 408

&lt;211&gt; 299

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 408

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 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr  
 20 25 30  
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met  
 35 40 45  
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala  
 50 55 60  
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser  
 65 70 75 80  
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln  
 85 90 95  
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu  
 100 105 110  
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val  
 115 120 125  
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile  
 130 135 140  
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly  
 145 150 155 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile  
 165 170 175  
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys  
 180 185 190  
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly  
 195 200 205  
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala  
 210 215 220  
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly  
 225 230 235 240  
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile  
 245 250 255  
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val  
 260 265 270  
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val  
 275 280 285  
 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp  
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 <223> RXC01158

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 Met Ser Ile Val Glu  
 1 5  
 cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163  
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile  
 10 15 20  
 ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211  
 Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp  
 25 30 35  
 cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg ?  
 Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu  
 40 45 50  
 cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa  
 Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu  
 55 60 65

ctc gca acc ggc ccg ttt gat	cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp	Pro Phe Met Leu Arg Leu Lys Val Ala	
70	80	85
gcg ttg gtg ggt atg gtt ctt	ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu	Gly Ser Pro Val Trp Leu Ser Gln Leu	
90	95	100
tgg ggc ttt atc acc cca ggt	ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly	Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105	110	115
gca atc ttc gtc acg att gct	gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala	Val Val Leu Phe Val Gly Gly Ala Val	
120	125	130
ctt gcg tac ttc gtc gtt gca	tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala	Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135	140	145
ggt gga gac acc cag gca gcg	gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala	Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150	155	160
ttc ttg ctc gcg ttg ttg gcg	att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala	Ile Phe Gly Val Ser Phe Glu Val Pro	
170	175	180
ctg gtg atc ggc atg ctc aac	att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn	Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185	190	195
att aaa gat aag cga cgc atg	atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met	Ile Ile Met Ile Leu Phe Val Phe Ala	
200	205	210
gct ttc atg aca ccc ggc cag	gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln	Asp Pro Phe Thr Met Leu Val Leu Ala	
215	220	225
ctt tca ctc acc gtt ctg gta	gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val	Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230	235	240
aac gac aaa cgc cgg gac aag	aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys	Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250	255	260
gac ctc tct gca tca cca ctg	gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu	Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265	270	275
cca agc cca gtc gaa acc cca	gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro	Glu Ala Val Glu Pro Ser Arg Met Leu	
280	285	290
aac cca agt ggg gag gcg tcg	ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser	Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295	300	305

ttc ggt gac gtg ctc tagggcctag ccagggtaccc tta  
 1065  
 Phe Gly Asp Val Leu  
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<210> 410

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

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Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp  
 35 40 45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser  
 50 55 60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu  
 65 70 75 80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val  
 85 90 95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn  
 100 105 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe  
 115 120 125

Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu  
 130 135 140

Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly  
 145 150 155 160

Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val  
 165 170 175

Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile  
 180 185 190

Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile  
 195 200 205

Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr  
 210 215 220

Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu  
 225 230 235 240

Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu  
 245 250 255

Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

260	265	270
Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu		
275	280	285
Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys		
290	295	300
Pro Gly Arg Ala Asp Phe Gly Asp Val Leu		
305	310	

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 <211> 1413  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1390)  
 <223> RXA02458

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 Met Val Phe Val Ser  
 1 5  
 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163  
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly  
 10 15 20  
 ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac 211  
 Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn  
 25 30 35  
 cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att 259  
 Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile  
 40 45 50  
 gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc 307  
 Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg  
 55 60 65  
 agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt 355  
 Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val  
 70 75 80 85  
 gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt 403  
 Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly  
 90 95 100  
 acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct 451  
 Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro  
 105 110 115  
 gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc 499  
 Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser  
 120 125 130

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt cgg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931
Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile	
265 270 275	
cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
280 285 290	
ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc	
1027	
Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly	
295 300 305	
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1075	
Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala	
310 315 320 325	
gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct	
1123	
Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala	
330 335 340	
cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag	
1171	
His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu	
345 350 355	

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg  
 1219  
 Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu  
           360                                  365                                  370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat  
 1267  
 Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp  
           375                                  380                                  385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc  
 1315  
 His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly  
 390                                  395                                  400                                  405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt  
 1363  
 Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe  
                                   410                                  415                                  420

gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat  
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                                   425                                  430

ccg  
 1413

<210> 412  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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                                   20                                  25                                  30  
 Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr  
                                   35                                  40                                  45  
 Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met  
           50                                  55                                  60  
 Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val  
   65                                  70                                  75                                  80  
 Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu  
                                   85                                  90                                  95  
 Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala  
                                   100                                  105                                  110  
 Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val  
           115                                  120                                  125  
 Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu  
   130                                  135                                  140

Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro  
 145 150 155 160  
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val  
 165 170 175  
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val  
 180 185 190  
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr  
 195 200 205  
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn  
 210 215 220  
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile  
 225 230 235 240  
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Ala Val  
 245 250 255  
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln  
 260 265 270  
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val  
 275 280 285  
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro  
 290 295 300  
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu  
 305 310 315 320  
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg  
 325 330 335  
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala  
 340 345 350  
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu  
 355 360 365  
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp  
 370 375 380  
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly  
 385 390 395 400  
 Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys  
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 Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly  
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&lt;210&gt; 413

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

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 <223> RXA02790

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 Met Glu Pro Val Tyr  
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gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163  
 Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
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ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211  
 Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
 25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259  
 Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val  
 40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307  
 Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu  
 55 60 65

gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355  
 Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser  
 70 75 80 85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403  
 Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln  
 90 95 100

gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451  
 Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp  
 105 110 115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499  
 Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp  
 120 125 130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547  
 Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile  
 135 140 145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595  
 Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu  
 150 155 160 165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643  
 Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val  
 170 175 180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691  
 Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys  
 185 190 195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	Val	Val	Asp	Pro	Ser	
	200						205					210				
aac	gac	gcc	cag	gga	atc	ctc	acc	gat	ctg	atc	acg	cga	tca	gca	aac	787
Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	Thr	Arg	Ser	Ala	Asn	
	215					220					225					
cat	ttc	caa	gaa	acc	gac	atc	acg	ggc	cgt	gca	gat	gcc	atc	gga	ctt	835
His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu	
	230				235					240					245	
act	cca	tat	gag	ctg	gtc	acc	gca	gca	tct	tta	atc	gag	cgc	gaa	gca	883
Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala	
				250					255					260		
cca	gca	gga	gat	ttt	gat	aag	gtc	gcc	cgc	gtc	atc	ttg	aac	cgt	ctc	931
Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	Ile	Leu	Asn	Arg	Leu	
			265					270					275			
gcc	gag	cca	atg	cag	ctg	caa	ttc	gac	tcc	acc	gtc	aac	tac	ggg	ctg	979
Ala	Glu	Pro	Met	Gln	Leu	Gln	Phe	Asp	Ser	Thr	Val	Asn	Tyr	Gly	Leu	
		280					285					290				
tct	gaa	caa	gaa	gta	gca	acc	acc	gac	gaa	gac	cgt	cag	acc	gtc	acc	
1027																
Ser	Glu	Gln	Glu	Val	Ala	Thr	Thr	Asp	Glu	Asp	Arg	Gln	Thr	Val	Thr	
	295					300					305					
cca	tgg	aac	act	tac	gcc	atg	gac	ggc	ctg	cca	caa	acc	ccc	atc	gcc	
1075																
Pro	Trp	Asn	Thr	Tyr	Ala	Met	Asp	Gly	Leu	Pro	Gln	Thr	Pro	Ile	Ala	
310					315					320					325	
gca	gta	tcc	acc	gaa	gca	ctc	caa	gcc	atg	gaa	aac	cct	gca	gaa	gga	
1123																
Ala	Val	Ser	Thr	Glu	Ala	Leu	Gln	Ala	Met	Glu	Asn	Pro	Ala	Glu	Gly	
				330					335					340		
aac	tgg	ctg	tac	ttt	gtc	acc	atc	gac	acc	gat	gga	acc	acc	gtg	ttc	
1171																
Asn	Trp	Leu	Tyr	Phe	Val	Thr	Ile	Asp	Thr	Asp	Gly	Thr	Thr	Val	Phe	
			345					350					355			
aac	gac	acc	ttc	gaa	gag	cac	gaa	gcc	gac	att	gag	caa	gct	ttg	aac	
1219																
Asn	Asp	Thr	Phe	Glu	Glu	His	Glu	Ala	Asp	Ile	Glu	Gln	Ala	Leu	Asn	
		360					365					370				
agt	ggc	gtt	cta	gac	agc	aac	cga	taaggatcag	cgaataaaaat	tgg						
1266																
Ser	Gly	Val	Leu	Asp	Ser	Asn	Arg									
	375					380										
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<213>	Corynebacterium glutamicum															
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Ala Thr Ser Asn 35	Arg Thr Pro His	Asp Tyr Glu Gly 40	Ser Gly Asn Gly 45
Val Val Gln Leu 50	Val Glu Ile Pro	Glu Gly Ser Ser 55	Ile Ser Glu Leu 60
Gly Pro Glu Leu 65	Glu Glu Arg Asp 70	Ile Val Ala Thr 75	Asn Ser Ala Phe 80
Gln Thr Ala Ala 85	Ser Asn Asn Pro	Asn Ala Gly Ser 90	Val Gln Pro Gly 95
Phe Tyr Arg Leu 100	Gln Glu Gln Met	Asn Ala Ala Ala 105	Val Ser Ala 110
Leu Leu Asp Pro 115	Asp Asn Gln Val	Asp Leu Leu Asp 120	Ile His Gly Gly 125
Ala Thr Leu Met 130	Asp Val Thr Val	Val Gly Gly Asn 135	Thr Arg Ala Gly 140
Ile Tyr Ser Gln 145	Ile Ala Ala Val	Thr Cys Thr Glu 150	Gly Ser Ala Asn 155
Cys Ile Thr Ala 165	Glu Asp Leu Gln	Gln Val Ala Ser 170	Thr Val Ser Pro 175
Ala Glu Leu Gly 180	Val Pro Asp Trp	Ala Ile Ala Ala 185	Val Glu Ala Arg 190
Gly Thr Asp Pro 195	Lys Arg Leu Glu	Gly Leu Ile Met 200	Pro Gly Gln Tyr 205
Val Val Asp Pro 210	Ser Asn Asp Ala	Gln Gly Ile Leu 215	Thr Asp Leu Ile 220
Thr Arg Ser Ala 225	Asn His Phe Gln	Glu Thr Asp Ile 230	Thr Gly Arg Ala 235
Asp Ala Ile Gly 245	Leu Thr Pro Tyr	Glu Leu Val Thr 250	Ala Ala Ser Leu 255
Ile Glu Arg Glu 260	Ala Pro Ala Gly	Asp Phe Asp Lys 265	Val Ala Arg Val 270
Ile Leu Asn Arg 275	Leu Ala Glu Pro	Met Gln Leu Gln 280	Phe Asp Ser Thr 285
Val Asn Tyr Gly 290	Leu Ser Glu Gln	Glu Val Ala Thr 295	Thr Thr Asp Glu 300
Arg Gln Thr Val 305	Thr Pro Trp Asn	Thr Tyr Ala Met 310	Asp Gly Leu Pro 315
Gln Thr Pro Ile 325	Ala Ala Val Ser	Thr Glu Ala Leu 330	Gln Ala Met Glu 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
 370 375 380

<210> 415

<211> 644

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

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 Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro  
 1 5 10 15

gcg tac aac cct gcg att gcg cat gtg cag ccg gtt cgc cag gcg ctg 96  
 Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
 20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144  
 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
 35 40 45

cgc ccg gag cgt cag atc atg ggc gtg gcc aat gcc aat cat gga cag 192  
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
 50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt aca cgc gcg ctt gtt 240  
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
 65 70 75 80

gtg cat ggc gca ggc acc gat gag atc gca gtc cac ggc acc acc ttg 288  
 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
 85 90 95

gtg tgg gag ctt aaa gaa gac ggc acc atc gag cat -tac acc atc gag 336  
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
 100 105 110

cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384  
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
 115 120 125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432  
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
 130 135 140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480  
 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
 145 150 155 160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528  
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                     165                    170                    175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576  
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
                     180                    185                    190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621  
 Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
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tagtaataat ctgcccacag tgt 644

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<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu  
                     20                    25                    30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
                     35                    40                    45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
                     50                    55                    60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
   65                    70                    75                    80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
                     85                    90                    95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
                     100                    105                    110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
                     115                    120                    125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
                     130                    135                    140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
   145                    150                    155                    160

Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
                     165                    170                    175

Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala  
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Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
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<210> 417  
 <211> 611  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(588)  
 <223> FRXA00954

<400> 417  
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 Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro  
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 gtt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca 96  
 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
 20 25 30  
 ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat 144  
 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
 35 40 45  
 gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt 192  
 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
 50 55 60  
 aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc 240  
 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
 65 70 75 80  
 cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag 288  
 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
 85 90 95  
 cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt 336  
 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
 100 105 110  
 gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc 384  
 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
 115 120 125  
 gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct 432  
 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
 130 135 140 -  
 gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg 480  
 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
 145 150 155 160  
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528  
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
 165 170 175  
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576  
 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
 180 185 190  
 tct tcc aat gac tagtaataat ctgcccacag tgt 611

Ser Ser Asn Asp  
195

<210> 418  
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Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
35 40 45  
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
50 55 60  
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
65 70 75 80  
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
85 90 95  
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
100 105 110  
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
115 120 125  
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
130 135 140  
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
145 150 155 160  
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
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Ser Ser Asn Asp  
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<222> (101)..(1654)  
<223> RXN00957

<400> 419

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Met Ser Thr Asn Pro  
1 5  
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163  
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu  
10 15 20  
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211  
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu  
25 30 35  
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259  
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu  
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aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307  
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln  
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Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln  
70 75 80 85  
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403  
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser  
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Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu  
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Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu  
120 125 130  
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547  
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu  
135 140 145  
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595  
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln  
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ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643  
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr  
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gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691  
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu  
185 190 195  
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739  
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu  
200 205 210  
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787  
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val  
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa	835
Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys	
230 235 240 245	
gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act	883
Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr	
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ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt	931
Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg	
265 270 275	
gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa	979
Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu	
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1123 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp	
330 335 340	
atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag	
1171 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu	
345 350 355	
cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg	
1219 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser	
360 365 370	
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1267 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr	
375 380 385	
tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca	
1315 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro	
390 395 400 405	
gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg	
1363 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr	
410 415 420	
ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc	
1411 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val	
425 430 435	

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc  
 1459  
 Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg  
           440                                  445                                  450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc  
 1507  
 Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val  
           455                                  460                                  465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat  
 1555  
 Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp  
 470                                  475                                  480                                  485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc  
 1603  
 Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala  
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 1651  
 Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile  
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 1677  
 Arg

<210> 420  
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 <213> Corynebacterium glutamicum

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 Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser  
                                   35                                  40                                  45  
 Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn  
                                   50                                  55                                  60  
 Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala  
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 Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe  
                                   85                                  90                                  95  
 Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala  
                                   100                                  105                                  110  
 Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr  
                                   115                                  120                                  125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe  
 130 135 140  
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr  
 145 150 155 160  
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn  
 165 170 175  
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly  
 180 185 190  
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala  
 195 200 205  
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp  
 210 215 220  
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln  
 225 230 235 240  
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val  
 245 250 255  
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala  
 260 265 270  
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile  
 275 280 285  
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro  
 290 295 300  
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr  
 305 310 315 320  
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile  
 325 330 335  
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala  
 340 345 350  
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp  
 355 360 365  
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu  
 370 375 380  
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr  
 385 390 395 400  
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys  
 405 410 415  
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu  
 420 425 430  
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala  
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile  
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala  
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu  
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Thr Leu Glu Val Ile Arg  
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<220>  
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 <223> FRXA00957

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aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac 96  
 Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp  
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atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc 144  
 Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala  
 35 40 45

cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac 192  
 Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp  
 50 55 60

gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac 240  
 Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp  
 65 70 75 80

ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc 288  
 Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg  
 85 90 95

acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac 336  
 Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr  
 100 105 110

caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc 384  
 Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe  
 115 120 125

gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc 432  
 Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe

130	135	140	
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ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly 180 185 190			576
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr 195 200 205			624
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg 210 215 220			672
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp 225 230 235 240			720
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg 245 250 255			768
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg 260 265 270			816
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala 275 280 285			864
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly 290 295 300			912
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile 305 310 315 320			960
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct 1008 Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala 325 330 335			
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acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct 1104 Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala 355 360 365			

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1151

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<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

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Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala  
35 40 45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp  
50 55 60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp  
65 70 75 80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg  
85 90 95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr  
100 105 110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe  
115 120 125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe  
130 135 140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala  
145 150 155 160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln  
165 170 175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly  
180 185 190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr  
195 200 205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg  
210 215 220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp  
225 230 235 240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg  
245 250 255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

260	265	270
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275	280	285
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly		
290	295	300
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile		
305	310	315
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala		
	325	330
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu		
	340	345
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala		
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Gly Ser Thr Leu Glu Val Ile Arg		
370	375	

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02687

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 Met Ser Asp Ala Pro 5  
 act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163  
 Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala 20  
 ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211  
 Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu 35  
 cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259  
 Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His 50  
 ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307  
 Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly 65  
 ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355  
 Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln 85  
 70 75 80 85

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg	403
Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg	
90 95 100	
cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt	451
Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val	
105 110 115	
ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc	499
Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala	
120 125 130	
atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc	547
Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala	
135 140 145	
gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc	595
Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu	
150 155 160 165	
ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc	643
Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala	
170 175 180	
cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg	691
Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro	
185 190 195	
acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca	739
Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro	
200 205 210	
ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac	787
Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp	
215 220 225	
ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac	835
Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr	
230 235 240 245	
cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc	883
Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala	
250 255 260	
gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc	931
Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val	
265 270 275	
ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac	979
Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp	
280 285 290	
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1027	
Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser	
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Glu Gly Arg Lys Leu Asn	
310 315	

<210> 424  
 <211> 315  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 424

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Phe	Thr	Glu	Glu	Ala	Leu	Tyr	Lys	Phe	Ala	Asp	Ala	Gly	Val	Phe	Gly
			20					25					30		
Asp	Gly	Glu	Ile	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Pro	Gln	Glu	Ala	Val
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Asp	Ala	Val	Arg	His	Gly	Thr	Ala	Gln	Phe	Ala	Val	Val	Ala	Ile	Glu
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Asn	Phe	Val	Asp	Gly	Pro	Val	Thr	Pro	Thr	Phe	Asp	Ala	Leu	Asp	Gln
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Gly	Ser	Asn	Val	Gln	Ile	Ile	Ala	Glu	Glu	Glu	Leu	Asp	Ile	Ala	Phe
				85					90					95	
Ser	Ile	Met	Val	Arg	Pro	Gly	Thr	Ser	Leu	Ala	Asp	Val	Lys	Thr	Leu
			100					105					110		
Ala	Thr	His	Pro	Val	Gly	Tyr	Gln	Gln	Val	Lys	Asn	Trp	Met	Ala	Thr
		115					120					125			
Thr	Ile	Pro	Asp	Ala	Met	Tyr	Leu	Ser	Ala	Ser	Ser	Asn	Gly	Ala	Gly
		130				135					140				
Ala	Gln	Met	Val	Ala	Glu	Gly	Thr	Ala	Asp	Ala	Ala	Ala	Ala	Pro	Ser
		145			150				155						160
Arg	Ala	Ala	Glu	Leu	Phe	Gly	Leu	Glu	Arg	Leu	Val	Asp	Asp	Val	Ala
				165					170					175	
Asp	Val	Arg	Gly	Ala	Arg	Thr	Arg	Phe	Val	Ala	Val	Gln	Ala	Gln	Ala
			180					185					190		
Ala	Val	Ser	Glu	Pro	Thr	Gly	His	Asp	Arg	Thr	Ser	Val	Ile	Phe	Ser
		195					200					205			
Leu	Pro	Asn	Val	Pro	Gly	Ser	Leu	Val	Arg	Ala	Leu	Asn	Glu	Phe	Ala
		210				215					220				
Ile	Arg	Gly	Val	Asp	Leu	Thr	Arg	Ile	Glu	Ser	Arg	Pro	Thr	Arg	Lys
		225			230					235					240
Val	Phe	Gly	Thr	Tyr	Arg	Phe	His	Leu	Asp	Ile	Ser	Gly	His	Ile	Arg
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Asp	Ile	Pro	Val	Ala	Glu	Ala	Leu	Arg	Ala	Leu	His	Leu	Gln	Ala	Glu
			260					265					270		
Glu	Leu	Val	Phe	Val	Gly	Ser	Trp	Pro	Ser	Asn	Arg	Ala	Glu	Asp	Ser
		275					280					285			

Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp  
 290 295 300

Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn  
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<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

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gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115  
 Met Leu Gly Met Leu  
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163  
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr  
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211  
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser  
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259  
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met  
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307  
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly  
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355  
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp  
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403  
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp  
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451  
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr  
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499  
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly  
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547  
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr  
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa	595
Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu	
150 155 160 165	
acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc	643
Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser	
170 175 180	
gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc	691
Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile	
185 190 195	
gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg	739
Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met	
200 205 210	
atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc	787
Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly	
215 220 225	
atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac	835
Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His	
230 235 240 245	
att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg	883
Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met	
250 255 260	
ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa	931
Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu	
265 270 275	
gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac	979
Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp	
280 285 290	
aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc	
1027	
Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly	
295 300 305	
atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att	
1075	
Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile	
310 315 320 325	
tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag	
1123	
Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys	
330 335 340	
gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc	
1171	
Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala	
345 350 355	
gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca	
1219	
Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala	
360 365 370	

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac  
 1267  
 Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn  
           375                                  380                                  385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt  
 1315  
 Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly  
           390                                  395                                  400                                  405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc  
 1353  
 Leu Glu Asp Gly Ala  
                                   410

<210> 426  
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 <213> Corynebacterium glutamicum

<400> 426  
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Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr  
                                   20                                  25                                  30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly  
                                   35                                  40                                  45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr  
                                   50                                  55                                  60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile  
                                   65                                  70                                  75                                  80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
                                   85                                  90                                  95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
                                   100                                  105                                  110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
                                   115                                  120                                  125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
                                   130                                  135                                  140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
                                   145                                  150                                  155                                  160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
                                   165                                  170                                  175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
                                   180                                  185                                  190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
                                   195                                  200                                  205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu  
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly  
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 405 410

<210> 427  
 <211> 1013  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(990)  
 <223> FRXA01698

<400> 427

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ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg	96
Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg	
20 25 30	
ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc	144
Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly	

35				40				45								
atg	ctc	aag	tac	gga	ttc	gat	gat	gcc	cgc	aac	gtg	ctg	gag	cgt	tct	192
Met	Leu	Lys	Tyr	Gly	Phe	Asp	Asp	Ala	Arg	Asn	Val	Leu	Glu	Arg	Ser	
	50					55					60					
tca	gcc	cgt	gag	acg	gca	gca	cgc	gtg	gca	gca	gca	acc	gtt	gcg	cgt	240
Ser	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Val	Ala	Ala	Ala	Thr	Val	Ala	Arg	
	65				70				75						80	
tcc	ttc	ctg	cgt	gaa	acc	ttg	ggc	gtg	gaa	gtg	ctt	tcc	cac	gta	att	288
Ser	Phe	Leu	Arg	Glu	Thr	Leu	Gly	Val	Glu	Val	Leu	Ser	His	Val	Ile	
				85					90					95		
tcc	att	ggc	gcg	tcc	gag	cct	tac	act	ggc	gcg	gag	cca	acc	ttt	gca	336
Ser	Ile	Gly	Ala	Ser	Glu	Pro	Tyr	Thr	Gly	Ala	Glu	Pro	Thr	Phe	Ala	
			100					105					110			
gat	att	caa	gca	atc	gat	gat	tcc	cca	gtt	cgt	gca	ttc	ggc	aaa	gac	384
Asp	Ile	Gln	Ala	Ile	Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp	
		115					120					125				
gct	gaa	gaa	tcc	atg	atc	gcg	gaa	atc	gag	gcc	gca	aag	aaa	gcc	ggc	432
Ala	Glu	Glu	Ser	Met	Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly	
	130					135					140					
gat	acc	ctc	ggc	ggc	atc	gtg	gaa	gtg	att	gtt	gaa	ggc	ctg	ccc	atc	480
Asp	Thr	Leu	Gly	Gly	Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile	
	145				150					155					160	
ggc	ttg	ggc	tca	cac	att	tct	ggc	gaa	gat	cgc	ctc	gat	gcg	cag	atc	528
Gly	Leu	Gly	Ser	His	Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile	
				165					170					175		
gca	gct	gca	ctc	atg	ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggc	576
Ala	Ala	Ala	Leu	Met	Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly	
			180					185					190			
gac	ggc	ttc	gaa	gaa	gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	624
Asp	Gly	Phe	Glu	Glu	Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu	
		195					200					205				
gtg	ttc	ctg	gat	gac	aac	ggc	gta	tac	cgc	aac	acc	aac	cgt	gca	ggc	672
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly	
	210					215					220					
ggc	ctc	gaa	ggc	ggc	atg	acc	aac	ggc	gaa	acc	ctg	cgc	gtt	cgt	gct	720
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala	
	225				230					235					240	
ggc	atg	aag	cca	att	tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	768
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp	
				245					250					255		
atg	gaa	aac	ggc	aag	gca	gca	acc	gga	atc	cac	cag	cgt	tcc	gac	gtg	816
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val	
			260					265					270			
tgc	gct	gtt	cca	gcc	gcc	ggc	gtc	gtt	gca	gaa	gca	atg	gtc	acc	ctg	864
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu	
		275					280					285				

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa  
 1010  
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 325 330

ttc  
 1013

<210> 428  
 <211> 330  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 428  
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
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Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
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Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu

195						200						205					
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly		
210						215					220						
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala		
225					230					235					240		
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp		
				245					250					255			
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val		
			260					265					270				
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu		
		275					280					285					
Val	Leu	Ala	Arg	Ala	Val	Leu	Gln	Lys	Phe	Gly	Gly	Asp	Ser	Leu	Ser		
	290					295					300						
Glu	Thr	Lys	Ser	Asn	Ile	Asp	Thr	Tyr	Leu	Lys	Asn	Ile	Glu	Glu	Arg		
305					310					315					320		
Met	Lys	Phe	Glu	Gly	Leu	Glu	Asp	Gly	Ala								
				325					330								

&lt;210&gt; 429

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; RXA01095

&lt;400&gt; 429

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ataaccttaa	acacagcatt	ggttggaagg	aggttggggc	atg	ggt	gca	aca	gag	115
				Met	Val	Ala	Thr	Glu	
				1				5	

aac	cgc	atg	ttg	atg	gaa	atc	gct	gcg	gaa	ata	tcg	gct	cgg	gaa	gca	163
Asn	Arg	Met	Leu	Met	Glu	Ile	Ala	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Ala	
			10					15						20		

acg	ctt	ggc	ttt	caa	gaa	gtc	aaa	act	aaa	tct	cga	tca	gca	ggc	ctc	211
Thr	Leu	Gly	Phe	Gln	Glu	Val	Lys	Thr	Lys	Ser	Arg	Ser	Ala	Gly	Leu	
			25				30						35			

acg	gcg	gct	ttc	gat	att	gct	tca	gtc	ttt	ttt	tcg	tct	gga	tgt	aat	259
Thr	Ala	Ala	Phe	Asp	Ile	Ala	Ser	Val	Phe	Phe	Ser	Ser	Gly	Cys	Asn	
		40				45						50				

gtc	gta	gtc	gcc	ttt	gat	cgt	ttt	gca	tcc	aat	tgg	tct	gat	cat	tcg	307
Val	Val	Val	Ala	Phe	Asp	Arg	Phe	Ala	Ser	Asn	Trp	Ser	Asp	His	Ser	
	55					60					65					

gat	cat	gtg	gac	tac	gct	gca	cag	ggt	gcg	ggc	ttt	ggc	gca	tca	atg	355
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Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met  
 70 75 80 85  
 ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403  
 Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp  
 90 95 100  
 atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451  
 Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp  
 105 110 115  
 ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499  
 Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile  
 120 125 130  
 gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547  
 Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu  
 135 140 145  
 tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595  
 Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser  
 150 155 160 165  
 gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643  
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr  
 170 175 180  
 gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691  
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro  
 185 190 195  
 gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739  
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg  
 200 205 210  
 att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787  
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala  
 215 220 225  
 cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835  
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr  
 230 235 240 245  
 aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt 883  
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg  
 250 255 260  
 tgaagaggtg ctctgtggtc agc 906

&lt;210&gt; 430

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile  
 1 5 10 15

Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser  
 20 25 30

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe  
           35                          40                          45  
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn  
           50                          55                          60  
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly  
           65                          70                          75                          80  
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp  
                           85                          90                          95  
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro  
                           100                          105                          110  
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala  
           115                          120                          125  
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu  
           130                          135                          140  
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met  
           145                          150                          155                          160  
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val  
                           165                          170                          175  
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly  
                           180                          185                          190  
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro  
           195                          200                          205  
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu  
           210                          215                          220  
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His  
           225                          230                          235                          240  
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro  
                           245                          250                          255  
 Ala Cys Pro Ser Arg  
                           260

&lt;210&gt; 431

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1522)

&lt;223&gt; RXA00955

&lt;400&gt; 431

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aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

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ctg	ccc	aca	gtg	ttg	gaa	agc	atc	gtc	gag	ggg	cgt	cgc	gga	cac	ctg						163
Leu	Pro	Thr	Val	Leu	Glu	Ser	Ile	Val	Glu	Gly	Arg	Arg	Gly	His	Leu						
				10					15					20							
gag	gaa	att	cgc	gct	cgc	atc	gct	cac	gtg	gat	gtg	gat	gcg	ctt	cca						211
Glu	Glu	Ile	Arg	Ala	Arg	Ile	Ala	His	Val	Asp	Val	Asp	Ala	Leu	Pro						
			25					30					35								
aaa	tcc	acc	cgt	tct	ctg	ttt	gat	tcc	ctc	aac	cag	ggg	agg	gga	ggg						259
Lys	Ser	Thr	Arg	Ser	Leu	Phe	Asp	Ser	Leu	Asn	Gln	Gly	Arg	Gly	Gly						
		40					45					50									
gcg	cgt	ttc	atc	atg	gag	tgc	aag	tcc	gca	tgc	cct	tct	ttg	gga	atg						307
Ala	Arg	Phe	Ile	Met	Glu	Cys	Lys	Ser	Ala	Ser	Pro	Ser	Leu	Gly	Met						
		55				60					65										
att	cgt	gag	cac	tac	cag	ccg	ggg	gaa	atc	gct	cgc	gtg	tac	tct	cgc						355
Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg						
	70				75					80					85						
tac	gcc	agc	ggc	att	tcc	gtg	ctg	tgc	gag	ccg	gat	cgt	ttt	ggg	ggc						403
Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly						
				90				95						100							
gat	tac	gat	cac	ctc	gct	acc	gtt	gcc	gct	acc	tct	cat	ctt	ccg	gtg						451
Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val						
			105					110					115								
ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt						499
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg						
		120					125					130									
tac	ttt	ggg	gct	gat	gcc	atc	ctg	ctc	atg	ctc	tct	gtg	ctt	gat	gat						547
Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp						
	135					140					145										
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat						595
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp						
	150				155					160				165							
atc	ctc	acc	gag	gtt	att	gat	gag	gag	gaa	gtc	gcc	cgc	gcc	atc	aag						643
Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys						
				170				175						180							
ctg	ggg	gcg	aag	atc	ttt	ggc	gtc	aac	cac	cgc	aac	ctg	cat	gat	ctg						691
Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu						
			185					190					195								
tcc	att	gat	ttg	gat	cgt	tca	cgt	cgc	ctg	tcc	aag	ctc	att	cca	gca						739
Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala						
		200					205					210									
gat	gcc	gtg	ctc	gtg	tct	gag	tct	ggc	gtg	cgc	gat	acc	gaa	acc	gtc						787
Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val						
	215					220				225											
cgc	cag	cta	ggg	ggg	cac	tcc	aat	gca	ttc	ctc	gtt	ggc	tcc	cag	ctg						835
Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu						

230		235		240		245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc							883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly							
		250		255		260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct							931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala							
		265		270		275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg							979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser							
		280		285		290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag							
1027							
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu							
		295		300		305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag							
1075							
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys							
		310		315		320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg							
1123							
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu							
		330		335		340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa							
1171							
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu							
		345		350		355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc							
1219							
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser							
		360		365		370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag							
1267							
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys							
		375		380		385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg							
1315							
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp							
		390		395		400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc							
1363							
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly							
		410		415		420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt							
1411							
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly							
		425		430		435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg							
1459							

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp  
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc  
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile  
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga  
 1545

Ser Thr Phe His Tyr  
 470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly  
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Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp  
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn  
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser  
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala  
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro  
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr  
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln  
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu  
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala  
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val  
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg  
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser  
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg  
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu  
 225 230 235 240  
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg  
 245 250 255  
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser  
 260 265 270  
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile  
 275 280 285  
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys  
 290 295 300  
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg  
 305 310 315 320  
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln  
 325 330 335  
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile  
 340 345 350  
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala  
 355 360 365  
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu  
 370 375 380  
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly  
 385 390 395 400  
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser  
 405 410 415  
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala  
 420 425 430  
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala  
 435 440 445  
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys  
 450 455 460  
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr  
 465 470

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 <223> RXA02814

<400> 433

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atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
  65          70          75          80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
          85          90          95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
          100          105          110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
          115          120          125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
          130          135          140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
          145          150          155

tcttaaaaca ccg 494

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&lt;210&gt; 434

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 434

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Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

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His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80  
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95  
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110  
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

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 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
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 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95  
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336  
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140

gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160

gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175

aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190

gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205

ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220

acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240

cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255

ttc ctg tcc ctc taaaagagtc agtaaaacct cga 803  
 Phe Leu Ser Leu  
 260

&lt;210&gt; 436

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
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Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30

Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45

Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60

Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80

Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
 Phe Leu Ser Leu  
 260

<210> 437  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA02093

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 Met Val Asn Tyr Val 5  
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 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163  
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn 20  
 10 15  
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211  
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn 35  
 25 30  
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
		40					45					50					
ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac	307	
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
	55					60					65						
aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag	355	
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
70					75					80					85		
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc	403	
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac	451	
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg	499	
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
		120					125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggt	ctg	agt	ggc	acc	547	
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
	135					140					145						
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggt	tct	gcg	cta	gct	tcc	cgt	tac	595	
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
					155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt	643	
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170				175						180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
	215					220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
	230				235				240						245		
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
				250				255						260			
gct	gcg	gag	gag	ttc	tcc	aag	taaattttctc	tcccctatttt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
				265													

&lt;210&gt; 438

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (928)

&lt;223&gt; RXA02791

&lt;400&gt; 439

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ggcgttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115  
 Leu Gly Ser His Ile  
 1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163  
 Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser  
 10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211  
 Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp  
 25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259  
 Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val  
 40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307  
 Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser  
 55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355  
 Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys  
 70 75 80 85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403  
 Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg  
 90 95 100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451  
 Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu  
 105 110 115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499  
 Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser  
 120 125 130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547  
 Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val  
 135 140 145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595  
 Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln  
 150 155 160 165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643  
 Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu  
 170 175 180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691  
 His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala  
 185 190 195

gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739  
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp  
           200                                  205                                  210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787  
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala  
           215                                  220                                  225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835  
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser  
 230                                  235                                  240                                  245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883  
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala  
                                   250                                  255                                  260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928  
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His  
                                   265                                  270                                  275

taagtcctccg ccacctcctc aac 951

&lt;210&gt; 440

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 440

Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile  
   1                                  5                                  10                                  15

Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu  
                                   20                                  25                                  30

Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met  
                                   35                                  40                                  45

Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser  
   50                                  55                                  60

Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val  
   65                                  70                                  75                                  80

Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr  
                                   85                                  90                                  95

Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly  
                                   100                                  105                                  110

Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala  
                                   115                                  120                                  125

Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu  
   130                                  135                                  140

Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg  
   145                                  150                                  155                                  160

Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala  
                                   165                                  170                                  175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser  
 180 185 190  
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile  
 195 200 205  
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val  
 210 215 220  
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met  
 225 230 235 240  
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp  
 245 250 255  
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile  
 260 265 270  
 Ser Glu Glu His  
 275

<210> 441  
 <211> 693  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(670)  
 <223> RXA01699

<400> 441  
 ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60  
 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115  
 Met Glu Arg Asn Glu 5  
 1  
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163  
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu 20  
 10 15  
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211  
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys 35  
 25 30  
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259  
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val 50  
 40 45  
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307  
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala 65  
 55 60  
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355  
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile 85  
 70 75 80  
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403

His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly  
 90 95 100  
 gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451  
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp 115  
 105 110  
 gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499  
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala 130  
 120 125  
 aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547  
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His 145  
 135 140  
 tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595  
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala 165  
 150 155 160  
 acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643  
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala 180  
 170 175  
 gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690  
 Ala Val Leu His His Leu Glu Ile Asp 190  
 185  
 tta 693

&lt;210&gt; 442

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 442

Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser  
 1 5 10 15  
 Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu  
 20 25 30  
 Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu  
 35 40 45  
 Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly  
 50 55 60  
 Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg  
 65 70 75 80  
 Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val  
 85 90 95  
 Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu  
 100 105 110  
 Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly  
 115 120 125  
 Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

130	135	140	
Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu			
145	150	155	160
Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro			
	165	170	175
Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp			
	180	185	190

<210> 443  
 <211> 959  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (97)..(936)  
 <223> RXA00952

<400> 443  
 catcctcgtc tccctatccg gccgtggcga caaggacgtt gaccacgtgc gccgcaccct 60  
 cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat 114  
 Met Ser Arg Tyr Asp Asp  
 1 5  
 ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162  
 Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe  
 10 15 20  
 atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210  
 Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser  
 25 30 35  
 aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258  
 Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe  
 40 45 50  
 tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306  
 Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg  
 55 60 65 70  
 gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354  
 Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys  
 75 80 85  
 cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402  
 Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr  
 90 95 100  
 ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450  
 Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe  
 105 110 115  
 gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498  
 Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg  
 120 125 130

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546  
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro  
 135 140 145 150  
 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594  
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val  
 155 160 165  
 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642  
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val  
 170 175 180  
 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690  
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val  
 185 190 195  
 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738  
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly  
 200 205 210  
 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786  
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser  
 215 220 225 230  
 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834  
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys  
 235 240 245  
 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882  
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu  
 250 255 260  
 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930  
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys  
 265 270 275  
 aag gtt taggccttta aatgtggcaa tgt 959  
 Lys Val  
 280

&lt;210&gt; 444

&lt;211&gt; 280

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu  
 1 5 10 15

Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu  
 20 25 30

Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu  
 35 40 45

Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val  
 50 55 60

Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser  
 65 70 75 80

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro  
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp  
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu  
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala  
130 135 140

Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu  
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala  
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp  
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro  
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala  
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys  
225 230 235 240

Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile  
245 250 255

Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala  
260 265 270

Met Lys Ala Ala Thr Lys Lys Val  
275 280

<210> 445  
<211> 1237  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1237)  
<223> RXN00956

<400> 445  
gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggtt aaataggatc atg act gaa aaa gaa 115  
Met Thr Glu Lys Glu  
1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931  
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly  
                   265                                  270                                  275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979  
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly  
                   280                                  285                                  290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc  
 1027  
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser  
                   295                                  300                                  305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac  
 1075  
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His  
 310                                  315                                  320                                  325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac  
 1123  
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp  
                                   330                                  335                                  340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc  
 1171  
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile  
                                   345                                  350                                  355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc  
 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
                   360                                  365                                  370

gcc aag acc gcc gaa gta  
 1237  
 Ala Lys Thr Ala Glu Val  
                   375

<210> 446

<211> 379

<212> PRT

<213> Corynebacterium glutamicum

<400> 446

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
           1                                  5                                  10                                  15

Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
                   20                                  25                                  30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
                   35                                  40                                  45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
                   50                                  55                                  60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
           65                                  70                                  75                                  80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

85								90				95			
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg
			100					105					110		
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly
		115					120					125			
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val
	130					135					140				
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg
145					150					155					160
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly
				165					170					175	
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr
			180					185					190		
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro
		195					200					205			
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala
	210					215					220				
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val
225					230					235					240
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe
				245					250					255	
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu
			260					265					270		
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile
		275					280					285			
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly
	290					295					300				
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly
305					310					315					320
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr
				325					330					335	
Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala
			340					345					350		
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala
		355					360					365			
Tyr	Ala	Leu	Lys	Arg	Ala	Lys	Thr	Ala	Glu	Val					
	370					375									

&lt;210&gt; 447

&lt;211&gt; 1231

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1231)

&lt;223&gt; FRXA00956

&lt;400&gt; 447

gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115  
 Met Thr Glu Lys Glu  
 1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
 10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211  
 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu  
 25 30 35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259  
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu  
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307  
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu  
 55 60 65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355  
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile  
 70 75 80 85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403  
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn  
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451  
 Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg  
 105 110 115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499  
 Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu  
 120 125 130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547  
 Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys  
 135 140 145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595  
 Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly  
 150 155 160 165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643  
 Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala  
 170 175 180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691  
 Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His  
 185 190 195

tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	
gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc	931
Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly	
265 270 275	
aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc	979
Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly	
280 285 290	
acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc	
1027	
Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser	
295 300 305	
tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac	
1075	
Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His	
310 315 320 325	
gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac	
1123	
Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp	
330 335 340	
gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc	
1171	
Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile	
345 350 355	
atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc	
1219	
Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg	
360 365 370	
gcc aag acc gcc	
1231	
Ala Lys Thr Ala	
375	

&lt;210&gt; 448

&lt;211&gt; 377

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 448

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
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 Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
 20 25 30  
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
 35 40 45  
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
 50 55 60  
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
 65 70 75 80  
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly  
 85 90 95  
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg  
 100 105 110  
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly  
 115 120 125  
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val  
 130 135 140  
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg  
 145 150 155 160  
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly  
 165 170 175  
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr  
 180 185 190  
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro  
 195 200 205  
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala  
 210 215 220  
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val  
 225 230 235 240  
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe  
 245 250 255  
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu  
 260 265 270  
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile  
 275 280 285  
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly  
 290 295 300  
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly  
 305 310 315 320  
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr

	325		330		335
Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala					
	340		345		350
Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala					
	355		360		365
Tyr Ala Leu Lys Arg Ala Lys Thr Ala					
	370		375		

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1378)  
 <223> RXA00064

<400> 449  
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 ggtccgtcta ttttgccacc acatgcggag gtacgcagtt atg agt tca gtt tcg 115  
 Met Ser Ser Val Ser  
 1 5  
 ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att 163  
 Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile  
 10 15 20  
 aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt 211  
 Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu  
 25 30 35  
 act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg 259  
 Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu  
 40 45 50  
 ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat 307  
 Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp  
 55 60 65  
 gtc cgt aac tat ggc ggg ctg gat ggc atc gtt gat att cgc cag att 355  
 Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val Asp Ile Arg Gln Ile  
 70 75 80 85  
 tgg gcg gat ttg ctg ggt gtt cct gtg gag cag gtc ttg gcg ggg gat 403  
 Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln Val Leu Ala Gly Asp  
 90 95 100  
 gct tcg agc ttg aac atc atg ttt gat gtg atc agc tgg tcg tac att 451  
 Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile Ser Trp Ser Tyr Ile  
 105 110 115  
 ttc ggt aac aat gat tcg gtt cag cct tgg tcg aag gaa gaa acc gtt 499  
 Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser Lys Glu Glu Thr Val  
 120 125 130

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg	547
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr	
135 140 145	
gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc	595
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly	
150 155 160 165	
cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag	643
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys	
170 175 180	
ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg	691
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val	
185 190 195	
aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg	739
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro	
200 205 210	
gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc	787
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr	
215 220 225	
gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct	835
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala	
230 235 240 245	
ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act	883
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr	
250 255 260	
ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc	931
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg	
265 270 275	
aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag	979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys	
280 285 290	
gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg	
1027	
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val	
295 300 305	
cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac	
1075	
Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn	
310 315 320 325	
aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg	
1123	
Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala	
330 335 340	
cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt	
1171	
Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val	
345 350 355	

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc  
 1219  
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile  
           360                                  365                                  370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag  
 1267  
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu  
           375                                  380                                  385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt  
 1315  
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu  
           390                                  395                                  400                                  405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg  
 1363  
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala  
                                   410                                  415                                  420

gag cat tac gct aac taaaagtgaac tacagcggag aca  
 1401  
 Glu His Tyr Ala Asn  
                                   425

<210> 450

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu  
       1                                  5                                  10                                  15

Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn  
                                   20                                  25                                  30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp  
                                   35                                  40                                  45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala  
                                   50                                  55                                  60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val  
                                   65                                  70                                  75                                  80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln  
                                   85                                  90                                  95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile  
                                   100                                  105                                  110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser  
                                   115                                  120                                  125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg  
                                   130                                  135                                  140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro  
                                   145                                  150                                  155                                  160

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys  
 165 170 175  
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro  
 180 185 190  
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met  
 195 200 205  
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala  
 210 215 220  
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly  
 225 230 235 240  
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser  
 245 250 255  
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr  
 260 265 270  
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly  
 275 280 285  
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly  
 290 295 300  
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu  
 305 310 315 320  
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala  
 325 330 335  
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile  
 340 345 350  
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala  
 355 360 365  
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu  
 370 375 380  
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro  
 385 390 395 400  
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val  
 405 410 415  
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn  
 420 425

&lt;210&gt; 451

&lt;211&gt; 1143

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1120)

&lt;223&gt; RXN00448

&lt;400&gt; 451

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ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtggt 60

catagagata accgtagtag gtatgtgccca cacttggtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                55                60                65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
                70                75                80                85

gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
                90                95                100

gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
                105                110                115

cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
                120                125                130

agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
                135                140                145

ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
                150                155                160                165

atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
                170                175                180

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
                185                190                195

cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
                200                205                210

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ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787  
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser  
 215 220 225

acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835  
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu  
 230 235 240 245

agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883  
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile  
 250 255 260

ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931  
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu  
 265 270 275

caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979  
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg  
 280 285 290

tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca  
 1027  
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser  
 295 300 305

tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag  
 1075  
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys  
 310 315 320 325

cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc  
 1120  
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
 330 335 340

tagttttatc ggctgatgat tct  
 1143

<210> 452  
 <211> 340  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 452  
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 Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser  
 20 25 30  
 Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp  
 35 40 45  
 Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala  
 50 55 60  
 Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile  
 65 70 75 80  
 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe

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<210> 453
<211> 689
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(666)
<223> FRXA00448
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&lt;400&gt; 453

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Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser		
1				5					10					15			
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc		96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe		
			20					25					30				
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc		144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile		
		35					40					45					
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc		192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val		
	50					55					60						
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat		240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His		
65					70					75					80		
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggt	gac	aac	ggt		288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly		
				85					90					95			
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc		336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr		
			100					105					110				
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc		384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser		
		115					120					125					
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc		432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu		
	130					135					140						
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa		480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln		
145				150					155						160		
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc		528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser		
				165					170					175			
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc		576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser		
			180					185					190				
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag		624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln		
		195				200						205					
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc				666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe				
	210					215					220						
tagttttatc	ggctgatgat	tct															689

&lt;210&gt; 454

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 454

Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser  
 1 5 10 15

Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe  
 20 25 30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile  
 35 40 45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val  
 50 55 60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His  
 65 70 75 80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly  
 85 90 95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr  
 100 105 110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser  
 115 120 125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu  
 130 135 140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln  
 145 150 155 160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser  
 165 170 175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser  
 180 185 190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln  
 195 200 205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
 210 215 220

&lt;210&gt; 455

&lt;211&gt; 346

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(346)

&lt;223&gt; FRXA00452

&lt;400&gt; 455

ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtgtt 60

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catagagata accgtagtag gtatgtgccca cacttggtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                55                60                65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
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<210> 456  
 <211> 82  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
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Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
                35                40                45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
  50                55                60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
  65                70                75                80

Asp Ser

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<210> 457  
 <211> 1248  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101) .. (1225)  
 <223> RXA00584

<400> 457

667

tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835  
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn  
 230 235 240 245  
  
 tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883  
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala  
 250 255 260  
  
 gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931  
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275  
  
 atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979  
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
 280 285 290  
  
 gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa  
 1027  
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305  
  
 gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag  
 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325  
  
 aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg  
 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340  
  
 tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc  
 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355  
  
 gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca  
 1219  
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala  
 360 365 370  
  
 gcc aag taattaaggg cgctagactg tta  
 1248  
 Ala Lys  
 375

&lt;210&gt; 458

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
 1 5 10 15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35					40					45					
Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe
50					55					60					
Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val
65					70					75					80
His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu
				85					90					95	
Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe
			100					105					110		
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro
		115					120					125			
His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg
	130					135					140				
Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu
145					150					155					160
Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp
				165					170					175	
Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu
			180					185					190		
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly
		195					200					205			
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His
	210					215					220				
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr
225					230					235					240
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly
				245					250					255	
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly
			260					265					270		
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys
		275					280					285			
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile
	290					295					300				
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu
305					310					315					320
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly
				325					330					335	
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp
			340				345						350		
Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg
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Glu Arg Arg Ala Ala Ala Lys  
370 375

<210> 459  
<211> 1983  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1960)  
<223> RXA00579

<400> 459  
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Met Arg Val Leu Ile 5  
att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163  
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu 20  
gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211  
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile 35  
gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259  
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His 50  
gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307  
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg 65  
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355  
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala 85  
ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403  
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly 100  
gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451  
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile 115  
cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499  
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg 130  
ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547  
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile 145  
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595  
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggg gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt	931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	
ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa	
1027	
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	
1075	
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
310 315 320 325	
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct	
1123	
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
330 335 340	
gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat	
1171	
Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr	
345 350 355	
ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg	
1219	
Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser	
360 365 370	
tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc	
1267	
Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala	

375	380	385
cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat 1315		
Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr 390 395 400 405		
ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg 1363		
Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro 410 415 420		
gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc 1411		
Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro 425 430 435		
att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459		
Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu 440 445 450		
atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg 1507		
Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu 455 460 465		
atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc 1555		
Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro 470 475 480 485		
acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca 1603		
Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr 490 495 500		
gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt 1651		
Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser 505 510 515		
ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt 1699		
Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly 520 525 530		
gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747		
Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala 535 540 545		
cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795		
Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly 550 555 560 565		
gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843		
Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn 570 575 580		

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt  
1983

Leu Phe Gly Val Glu Phe Pro  
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu  
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Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro  
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Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
195 200 205

Thr	Phe	Phe	Ala	His	Ser	Ser	His	Ala	Phe	Trp	Leu	Asp	Asp	Ala	Gln
210						215					220				
Gly	Thr	Ser	Tyr	Leu	Gly	Asp	Ala	Ser	Gly	Pro	Leu	Ala	Arg	Thr	Lys
225					230					235					240
Thr	His	Asn	Val	Gly	Glu	Gly	Asp	Phe	Phe	Thr	Trp	Leu	Lys	Glu	Asp
				245					250					255	
Leu	Ala	Ala	Asn	Ser	Val	Ala	Pro	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Trp
			260					265					270		
Val	Gly	Tyr	Val	Gly	Tyr	Glu	Leu	Lys	Ala	Glu	Ala	Gly	Ala	Arg	Ala
		275					280					285			
Ala	His	Thr	Ser	Ser	Leu	Pro	Asp	Ala	His	Leu	Ile	Phe	Ala	Asp	Arg
	290					295					300				
Ala	Ile	Ala	Val	Glu	Ser	Asp	Gln	Val	Arg	Leu	Leu	Ala	Leu	Gly	Glu
305					310					315					320
Gln	Asp	Glu	Trp	Phe	Glu	Glu	Thr	Ile	Lys	Lys	Leu	His	Asn	Leu	Val
				325					330					335	
Ala	Pro	Arg	Ile	Pro	Ala	Ser	Gly	His	Leu	Ala	Leu	Gln	Val	Arg	Asp
			340					345					350		
Ser	Lys	Asp	Glu	Tyr	Leu	Asp	Lys	Ile	Arg	Arg	Ala	Gln	Glu	Leu	Ile
		355					360					365			
Thr	Arg	Gly	Glu	Ser	Tyr	Glu	Ile	Cys	Leu	Thr	Thr	Lys	Leu	Gln	Gly
	370					375					380				
Thr	Thr	Asp	Val	Ala	Pro	Leu	Ala	Ala	Tyr	Leu	Ala	Leu	Arg	Gly	Ala
385					390					395					400
Asn	Pro	Thr	Ala	Tyr	Gly	Ala	Tyr	Leu	Gln	Leu	Gly	Asp	Thr	Ser	Ile
			405						410					415	
Leu	Ser	Ser	Ser	Pro	Glu	Arg	Phe	Ile	Thr	Ile	Asp	Ser	Ala	Gly	Tyr
			420					425					430		
Val	Glu	Ser	Lys	Pro	Ile	Lys	Gly	Thr	Arg	Pro	Arg	Gly	Arg	Thr	Ala
		435					440					445			
Gln	Glu	Asp	Gln	Glu	Ile	Ile	Ala	Glu	Leu	Arg	Ser	Asn	Pro	Lys	Asp
	450					455					460				
Arg	Ala	Glu	Asn	Leu	Met	Ile	Val	Asp	Leu	Val	Arg	Asn	Asp	Leu	Ala
465					470					475					480
Arg	Gly	Ala	Leu	Pro	Thr	Thr	Val	Lys	Thr	Ser	Lys	Leu	Phe	Asp	Val
				485					490					495	
Glu	Thr	Tyr	Ala	Thr	Val	His	Gln	Leu	Val	Ser	Thr	Val	Ser	Ala	Glu
			500					505					510		
Leu	Gly	Pro	Arg	Ser	Pro	Ile	Glu	Cys	Val	Arg	Ala	Ala	Phe	Pro	Gly
		515					520					525			

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp  
 530 535 540  
 Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
 545 550 555 560  
 Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
 565 570 575  
 Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu  
 580 585 590  
 Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser  
 595 600 605  
 Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro  
 610 615 620

<210> 461  
 <211> 747  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(724)  
 <223> RXA00958

<400> 461

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 Met Thr His Val Val  
 1 5  
 ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163  
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe  
 10 15 20  
 gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211  
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val  
 25 30 35  
 gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259  
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly  
 40 45 -50  
 cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307  
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg  
 55 60 65  
 aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355  
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala  
 70 75 80 85  
 ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403  
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His  
 90 95 100  
 ggc acc acc gac aac atg atc ctt act gat gca gg' gtg cag agc cct 451

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro  
 105 110 115  
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499  
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile  
 120 125 130  
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547  
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val  
 135 140 145  
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595  
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile  
 150 155 160 165  
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643  
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly  
 170 175 180  
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691  
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile  
 185 190 195  
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744  
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 200 205  
 tca 747

&lt;210&gt; 462

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn  
 1 5 10 15  
 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg  
 20 25 30  
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
 35 40 45  
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60  
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80  
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95  
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110  
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125  
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

130		135		140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr				
145		150		155 160
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp				
		165		170 175
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro				
		180		185 190
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn				
		195		200 205

<210> 463  
 <211> 469  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(469)  
 <223> RXN03007

<400> 463  
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 gaacagcttc tcgcgaacta ataaaaaaag gattttgattc atg act tct cca gca 115  
 Met Thr Ser Pro Ala 5  
 1  
 aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg 163  
 Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu 20  
 10 15  
 gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat 211  
 Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp 35  
 25 30  
 gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag 259  
 Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu 50  
 40 45  
 cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct 307  
 Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala 65  
 55 60  
 cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act 355  
 Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr 85  
 70 75 80  
 ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg 403  
 Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu 100  
 90 95  
 atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg 451  
 Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser

105

110

115

gtg agc tcc aag tcc ggc  
Val Ser Ser Lys Ser Gly  
120

469

&lt;210&gt; 464

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 464

Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn  
1 5 10 15

Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr  
20 25 30

Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile  
35 40 45

Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala  
50 55 60

Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu  
65 70 75 80

Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr  
85 90 95

Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys  
100 105 110

His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly  
115 120

&lt;210&gt; 465

&lt;211&gt; 564

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(541)

&lt;223&gt; RXN02918

&lt;400&gt; 465

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tgattctatt attgccaaat cagaaagcag gagagacccg atg agc gaa atc cta 115  
Met Ser Glu Ile Leu  
1 5

gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163  
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala  
10 15 20

ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211  
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His

	25	30	35	
acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc				259
Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr				
	40	45	50	
gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg				307
Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala				
	55	60	65	
cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg				355
Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu				
	70	75	80	85
ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc				403
Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser				
	90	95	100	
aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc				451
Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser				
	105	110	115	
cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct				499
Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser				
	120	125	130	
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac				541
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp				
	135	140	145	
taattgtctc ccatttaagg agt				564

&lt;210&gt; 466

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 466

Met Ser Glu Ile Leu Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr																
1				5				10						15		
Glu Glu Ala Thr Ala Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp																
			20					25						30		
Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu																
			35					40						45		
Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe																
			50					55						60		
Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr																
			65					70						75		80
Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg																
			85					90								95
Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys																
			100					105						110		
Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp																

115	120	125	
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser	Glu Glu Leu Arg Gly		
130	135	140	
Gln Leu Asp			
145			
<210> 467			
<211> 735			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(712)			
<223> RXN01116			
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acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt 115			
		Met Ala Ala Arg Val	
		1 5	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg 163			
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
10	15	20	
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt 211			
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
25	30	35	
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag 259			
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
40	45	50	
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt 307			
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
55	60	65	
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc 355			
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
70	75	80	85
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc 403			
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
90	95	100	
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag 451			
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
105	110	115	
ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc 499			
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
120	125	130	
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag 547			
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
135	140	145	

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595  
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val 165  
 150 155 160

acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643  
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu 180  
 170 175

atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691  
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr 195  
 185 190

gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735  
 Glu Ala Asp Phe Lys Val Ala 200

<210> 468

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn 15  
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Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly 30  
 20 25

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro 45  
 35 40

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys 60  
 50 55

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp 80  
 65 70 75

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly 95  
 85 90

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro 110  
 100 105

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly 125  
 115 120

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala 140  
 130 135

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys 160  
 145 150 155

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu 175  
 165 170

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu 190  
 180 185

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

200

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<220>  
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<222> (101) .. (853)  
<223> RXN01115
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agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163  
Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser  
10 15 20

aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259  
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser  
40 45 50

gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307  
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val  
55 60 65

ctg	gat	acc	ctc	gat	gac	ctg	ggt	gtc	gga	aac	ttc	ggc	gtc	atc	gga	355
Leu	Asp	Thr	Leu	Asp	Asp	Leu	Gly	Val	Gly	Asn	Phe	Gly	Val	Ile	Gly	
70					75					80					85	

cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403  
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp  
90 95 100

cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451  
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu  
105 110 115

ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499  
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr  
120 125 130

ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547  
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp  
135 140 145

ttg	gag	aac	aac	cca	gcg	tcc	cgc	gag	cac	ttc	gaa	gcc	atg	gtt	gcc	595
Leu	Glu	Asn	Asn	Pro	Ala	Ser	Arg	Glu	His	Phe	Glu	Ala	Met	Val	Ala	
150					155					160					165	

ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr  
 170 175 180  
 tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691  
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr  
 185 190 195  
 atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739  
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile  
 200 205 210  
 att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787  
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro  
 215 220 225  
 gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835  
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu  
 230 235 240 245  
 cta gca cag cat ttc gct taatgttgta ggcatgttca caa 876  
 Leu Ala Gln His Phe Ala  
 250

&lt;210&gt; 470

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu  
 1 5 10 15  
 Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln  
 20 25 30  
 Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg  
 35 40 45  
 Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp  
 50 55 60  
 Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn  
 65 70 75 80  
 Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu  
 85 90 95  
 Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala  
 100 105 110  
 Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys  
 115 120 125  
 Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp  
 130 135 140  
 Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe  
 145 150 155 160  
 Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys

	165		170		175
Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr	180		185		190
Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro	195		200		205
Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala	210		215		220
Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn	225		230		235
Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala	245		250		

<210> 471  
 <211> 1284  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1261)  
 <223> RXS00116

<400> 471  
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 tttgcgccacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115  
 Met Ser Asn Asp Phe  
 1 5  
 gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163  
 Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met  
 10 15 20  
 acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211  
 Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe  
 25 30 35  
 cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259  
 Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln  
 40 45 50  
 att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307  
 Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser  
 55 60 65  
 ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355  
 Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu  
 70 75 80 85  
 tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403  
 Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala  
 90 95 100  
 att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451  
 Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile

105								110				115				
ggt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala	
		120					125					130				
ggg	gcg	acg	cgg	gtg	gcg	ggt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp	
		135				140					145					
gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg	
		150			155					160					165	
atg	att	atc	ggt	aat	tcg	ccg	cat	aat	ccg	acg	ggt	tcg	gtg	ttt	tct	643
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser	
				170					175					180		
aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggt	ggt	gct	cgt	gcg	tat	gac	ttg	691
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu	
			185				190						195			
ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	ggt	ttt	gat	gat	cag	739
Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu	Val	Phe	Asp	Asp	Gln	
		200				205						210				
aag	cat	gtg	agt	gtc	gcg	aag	ctg	ccc	ggt	atg	tgg	gat	cgc	acg	gtg	787
Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met	Trp	Asp	Arg	Thr	Val	
		215				220				225						
acg	gtg	tcg	tcg	gcg	gcg	aaa	acg	ttc	aat	gtg	act	ggt	tgg	aag	acg	835
Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val	Thr	Gly	Trp	Lys	Thr	
		230			235					240				245		
ggg	tgg	gcg	ttg	gca	ccg	gag	ccg	ttg	ttg	gag	gcg	gtg	ttg	aag	gcg	883
Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu	Ala	Val	Leu	Lys	Ala	
				250			255						260			
aag	cag	ttt	atg	tct	tat	gtg	ggg	gct	aca	cct	ttt	cag	ccg	gct	gtg	931
Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro	Phe	Gln	Pro	Ala	Val	
			265				270					275				
gcg	cat	gcg	att	gaa	cat	gag	cag	aag	tgg	gtg	tca	aag	atg	tct	aag	979
Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val	Ser	Lys	Met	Ser	Lys	
			280			285						290				
ggg	ctt	gag	ctc	aag	cgg	gat	att	ttg	cgt	act	gcg	tta	gat	aag	gcg	
1027																
Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr	Ala	Leu	Asp	Lys	Ala	
		295				300					305					
ggg	ctg	aag	act	cat	gac	agt	atg	ggc	acg	tat	ttc	atc	gtt	gcg	gat	
1075																
Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr	Phe	Ile	Val	Ala	Asp	
		310			315					320				325		
att	ggg	gat	cgt	gat	ggt	gcg	gag	ttc	tgt	ttt	gag	ttg	att	gag	aag	
1123																
Ile	Gly	Asp	Arg	Asp	Gly	Ala	Glu	Phe	Cys	Phe	Glu	Leu	Ile	Glu	Lys	
				330			335							340		

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag  
 1171  
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys  
                   345                  350                  355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg  
 1219  
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr  
           360                  365                  370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta  
 1261  
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu  
           375                  380                  385

tagtttgaac aggttggttg ggg  
 1284

<210> 472  
 <211> 387  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 472  
 Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr  
   1                  5                  10                  15  
 Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn  
                   20                  25                  30  
 Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
           35                  40                  45  
 Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
   50                  55                  60  
 Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
   65                  70                  75                  80  
 Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
                   85                  90                  95  
 Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
           100                  105                  110  
 Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
   115                  120                  125  
 Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
   130                  135                  140  
 Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
   145                  150                  155                  160  
 Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
           165                  170                  175  
 Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
           180                  185                  190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
195 200 205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
210 215 220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
225 230 235 240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
245 250 255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
260 265 270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
275 280 285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
290 295 300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
305 310 315 320

Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys  
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Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile  
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Lys Lys Leu  
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<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> FRXA00116

<400> 473

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Met Thr Gln Arg Ala  
1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163  
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp  
10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211  
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly  
                   25                                  30                                  35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259  
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala  
                   40                                  45                                  50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307  
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp  
                   55                                  60                                  65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355  
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr  
                   70                                  75                                  80                                  85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403  
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro  
                                   90                                  95                                  100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451  
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg  
                   105                                  110                                  115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499  
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val  
                   120                                  125                                  130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547  
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val  
                   135                                  140                                  145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595  
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu  
                   150                                  155                                  160                                  165

aag cag ttg gcg 607  
 Lys Gln Leu Ala

&lt;210&gt; 474

&lt;211&gt; 169

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly  
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Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu  
                   20                                  25                                  30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala  
                   35                                  40                                  45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu  
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Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu  
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Leu Leu Arg Asp Ser																5
1																
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																163
Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile Ala Leu Val Met Ala																
10 15 20																
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																211
Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala Gln Leu Thr Pro Leu																
25 30 35																
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																259
Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln Phe Leu Gly Gly Glu																
40 45 50																
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag																307
Gly Gln Trp Leu Leu Ala Met Pro Ala His His Ile Ala Gly Met Gln																
55 60 65																
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat																355
Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu Pro Leu Ala Ile Asp																
70 75 80 85																
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa																403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Ala Glu																
90 95 100																

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 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
 105 110 115  
  
 tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
 120 125 130  
  
 ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
 135 140 145  
  
 att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
 150 155 160 165  
  
 tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
 170 175 180  
  
 gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
 185 190 195  
  
 att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
 200 205 210  
  
 gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
 215 220 225  
  
 ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
 230 235 240

tgc 843

<210> 476

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

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Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

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<212> DNA
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<222> (101) .. (994)
<223> RXS00393
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Met Ser His Thr Glu																
1 5																
ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc																163
Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg																
10 15 20																
ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt																211
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly																
25 30 35																
gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg																259
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala																
40 45 50																

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
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ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

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 1017  
 Ala Leu Ala Phe Ser  
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<210> 478  
 <211> 298  
 <212> PRT  
 <213> Corynebacterium glutamicum

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                   20                  25                  30  
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
           35                          40                  45  
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
       50                          55                  60  
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
   65                  70                  75                  80  
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
                   85                  90                  95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
                   100                  105                  110  
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
           115                          120                  125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
   130                          135                  140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
  145                  150                  155                  160  
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
                   165                  170                  175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
                   180                  185                  190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
           195                          200                  205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
   210                          215                  220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
  225                          230                  235                  240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
                   245                  250                  255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

260	265	270
Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala		
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Val Leu Thr Gly Leu Ala Leu Ala Phe Ser		
290	295	

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA00393

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 Met Ser His Thr Glu  
 1 5

ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg  
 10 15 20

ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
 25 30 35

gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259  
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
 40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307  
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp  
 55 60 65

tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355  
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
 70 75 80 85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451  
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595  
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met  
 150 155 160 165  
  
 gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
 170 175 180  
  
 gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
 185 190 195  
  
 aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
 200 205 210  
  
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
 215 220 225  
  
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
 230 235 240 245  
  
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
 250 255 260  
  
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser  
 265 270 275  
  
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979  
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 280 285 290

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 1005  
 His

<210> 480  
 <211> 294  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 480  
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 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
 35 40 45  
  
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
 50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
 65 70 75 80  
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
 85 90 95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
 100 105 110  
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
 130 135 140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
 145 150 155 160  
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
 165 170 175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
 180 185 190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
 210 215 220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
 225 230 235 240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
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 Cys Ser Arg Ala Trp His  
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<210> 481  
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 <212> DNA  
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 <223> RXS00446

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 Met Gly Ala Val Glu

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Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val	
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acg	gta	ggg	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala	
			25					30					35			
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu	
		40					45					50				
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile	
	55					60					65					
ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala	
	70				75					80					85	
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro	
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tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys	
			105					110					115			
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe	
		120					125					130				
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His	
	135					140					145					
gac	aac	gtg	att	ggg	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala	
150					155					160				165		
ggc	ttg	cgt	gtt	ggg	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala	
			170					175						180		
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala	
			185					190					195			
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val	
		200					205					210				
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggg	gct	787
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala	
	215					220					225					
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala	
230					235					240				245		

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
                   250                  255                  260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
                   265                  270                  275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
                   280                  285

tgc 987

<210> 482

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

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Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
                   20                  25                  30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
                   35                  40                  45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
                   50                  55                  60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
   65                  70                  75                  80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
                   85                  90                  95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
                   100                  105                  110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
                   115                  120                  125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu  
                   130                  135                  140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys  
   145                  150                  155                  160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala  
                   165                  170                  175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn  
                   180                  185                  190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
                   195                  200                  205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
 210 215 220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
 260 265 270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 275 280 285

<210> 483  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(522)  
 <223> FRXA00446

<400> 483  
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 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30  
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140  
 cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160  
 act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170  
 tagtctttgg cgttttgcgg tgc 545

<210> 484  
 <211> 174  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 484  
 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
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 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

<210> 485  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<400> 485																60
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gaagccaagc actagaagca atgttcagcc gtttcgcgctc atg cag atg ttg gac																115
Met Gln Met Leu Asp																
1 5																
cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc																163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys																
10 15 20																
gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca																211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala																
25 30 35																
gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt																259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly																
40 45 50																
gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat																307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr																
55 60 65																
gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca																355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser																
70 75 80 85																
ggc gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat																403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr																
90 95 100																
gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa																451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu																
105 110 115																
tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt																499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg																
120 125 130																
ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag																547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys																
135 140 145																
gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat																595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp																
150 155 160 165																
ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct																643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala																
170 175 180																
gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg																691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro																
185 190 195																
ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc																739

Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr  
 200 205 210  
 ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787  
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile  
 215 220 225  
 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835  
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu  
 230 235 240 245  
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883  
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe  
 250 255 260  
 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931  
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg  
 265 270 275  
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979  
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly  
 280 285 290  
 act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct  
 1027  
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser  
 295 300 305  
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa  
 1075  
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu  
 310 315 320 325  
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc  
 1123  
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly  
 330 335 340  
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att  
 1171  
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile  
 345 350 355  
 gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac  
 1217  
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 360 365  
 taggttagtt tcg  
 1230

&lt;210&gt; 486

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30  
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45  
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60  
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80  
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu  
 85 90 95  
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr  
 100 105 110  
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys  
 115 120 125  
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu  
 130 135 140  
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr  
 145 150 155 160  
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys  
 165 170 175  
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met  
 180 185 190  
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala  
 195 200 205  
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg  
 210 215 220  
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn  
 225 230 235 240  
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala  
 245 250 255  
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His  
 260 265 270  
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro  
 275 280 285  
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu  
 290 295 300  
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu  
 305 310 315 320  
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe  
 325 330 335  
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser



340

345

350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys  
355 360 365

Lys

**<210> 487**

<211> 657

**<212> DNA**

<213> Corynebacterium glutamicum

**<220>**

<221> CDS

**<222> (101) .. (634)**

<223> FRXA00618

<400> 487

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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115  
Met Ser Phe Gly Arg  
1 5

ccg	ctg	gca	act	gcg	cat	cag	ttt	tcc	aag	aac	gcc	atc	gtg	gtg	ggt	163
Pro	Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala	Ile	Val	Val	Gly	
				10					15					20		

acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211  
Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile  
25 30 35

atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259  
Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser  
40 45 50

ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307  
Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala  
55 60 65

ttc	act	ttg	gag	gct	ggg	gcc	gaa	ctt	gat	gcc	cac	gtt	gaa	gcg	tat	355
Phe	Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His	Val	Glu	Ala	Tyr	
70					75					80					85	

cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403  
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu  
 90 95 100

ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451  
Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val  
105 110 115

tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499  
Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp  
120 125 130

gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547  
Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu  
135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS  
 <222> (101)..(385)  
 <223> FRXA00627

<400> 489

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gaagccaagc actagaagca atgttcagcc gtttcgcgctc atg cag atg ttg gac 115
                                         Met Gln Met Leu Asp
                                         1                               5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10                               15                               20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25                               30                               35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40                               45                               50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55                               60                               65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                        70                               75                               80                               85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
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<210> 490  
 <211> 95  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 490

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Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
                        20                               25                               30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
                        35                               40                               45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
                        50                               55                               60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
                        65                               70                               75                               80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
                        85                               90                               95
  
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Phe	Val	Thr	Thr	Pro	Asn	Asn	Pro	Thr	Gly	Asp	Val	Thr	Ser	Leu	Asp	
				170					175					180		

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
330 335 340	
cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
345 350 355	
gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca	
1218 Ala Ala Glu Ile Ile Lys Leu Asn Leu	
360 365	
tga	
1221	

&lt;210&gt; 492

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 492

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Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
 1           5           10           15

Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
          20           25           30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
          35           40           45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
 50           55           60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
65           70           75           80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
          85           90           95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
          100           105           110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
          115           120           125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
          130           135           140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
145           150           155           160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
          165           170           175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
          180           185           190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
          195           200           205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
          210           215           220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
225           230           235           240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
          245           250           255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
          260           265           270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
          275           280           285

Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
          290           295           300

Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
305           310           315           320

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Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp  
 340 345 350

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<210> 493

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1729)

<223> RXS02315

<400> 493

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gaatcgtatc cgtacctgga gacgatctag actgttgtgc atg tcc agc acg cca 115  
 Met Ser Ser Thr Pro  
 1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163  
 Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val  
 10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211  
 Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu  
 25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259  
 Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu  
 40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307  
 Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg  
 55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355  
 Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu  
 70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403  
 Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu  
 90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451  
 Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr  
 105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499  
 Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile  
 120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547

Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly	
135						140					145					
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu	
150					155					160					165	
gtt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggc	gag	gca	gtt	gga	gca	tca	643
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser	
				170					175					180		
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggc	gag	gtg	acc	gtg	gac	ctg	ggg	691
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly	
			185					190					195			
gag	cac	acc	ctc	gtg	att	gcc	ggc	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly	
		200					205					210				
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr	
	215					220					225					
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val	
230					235					240					245	
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val	
				250					255					260		
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp	
			265					270					275			
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp	
		280					285					290				
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc	
1027																
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly	
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acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tcg	gca	gca	tca	gaa	ctt	
1075																
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu	
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gcg	gcc	gat	ggc	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggc	ttc	
1123																
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe	
				330					335					340		
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc	
1171																
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly	
			345					350					355			
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg	
1219																

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu  
 360 365 370  
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc  
 1267  
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val  
 375 380 385  
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 1315  
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala  
 390 395 400 405  
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc  
 1363  
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala  
 410 415 420  
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc  
 1411  
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile  
 425 430 435  
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac  
 1459  
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn  
 440 445 450  
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt  
 1507  
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly  
 455 460 465  
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc  
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 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser  
 470 475 480 485  
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac  
 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
 490 495 500  
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
 1651  
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
 505 510 515  
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca  
 1699  
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala  
 520 525 530  
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt  
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 Gln Gln Gln Ala Leu Met Asp Thr Val His  
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 1752

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 <213> Corynebacterium glutamicum

<400> 494

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Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
          35           40           45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
          50           55           60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65           70           75           80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
          85           90           95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
          100          105          110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
          115          120          125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
          130          135          140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
          145          150          155          160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
          165          170          175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
          180          185          190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
          195          200          205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
          210          215          220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
          225          230          235          240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
          245          250          255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
          260          265          270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
          275          280          285

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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
 290 295 300  
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
 305 310 315 320  
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn  
 325 330 335  
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
 340 345 350  
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile  
 355 360 365  
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe  
 370 375 380  
 Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile  
 385 390 395 400  
 Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala  
 405 410 415  
 Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile  
 420 425 430  
 Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr  
 435 440 445  
 Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu  
 450 455 460  
 Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr  
 465 470 475 480  
 Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu  
 485 490 495  
 His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp  
 500 505 510  
 Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg  
 515 520 525  
 Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His  
 530 535 540 --

&lt;210&gt; 495

&lt;211&gt; 1434

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1411)

&lt;223&gt; RXS02550

&lt;400&gt; 495

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715

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835  
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg  
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883  
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro  
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931  
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val  
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979  
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr  
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc  
 1027  
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu  
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga  
 1075  
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly  
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa  
 1123  
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu  
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc  
 1171  
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser  
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc  
 1219  
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro  
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc  
 1267  
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu  
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca  
 1315  
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
 1363  
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag  
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 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
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1434

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<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

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Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu  
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly  
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe  
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr  
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala  
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val  
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr  
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro  
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro  
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu  
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile  
195 200 205

Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu  
210 215 220

Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp  
225 230 235 240

Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu  
245 250 255

Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser  
260 265 270

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
 275 280 285  
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
 290 295 300  
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
 305 310 315 320  
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
 325 330 335  
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
 340 345 350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
 355 360 365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
 370 375 380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
 385 390 395 400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
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 Ser Thr Tyr Lys Gln  
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 Met Ser Asn Tyr Ser  
 1 5  
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163  
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe  
 10 15 20  
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211  
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
 25 30 35  
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259  
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

40	45	50	
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gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
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gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct  
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr  
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aaa  
1080

<210> 498

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

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Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg  
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140 -

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210	215	220
Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp 225 230 235 240		
His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn 245 250 255		
Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu 260 265 270		
Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr 275 280 285		
Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe 290 295 300		
Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr 305 310 315		

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXS02908

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 gtgactggtc gcgtggatac ccgtcattga ttccgggtgga ttg aag ttg cac cca 115  
 Leu Lys Leu His Pro  
 1 5  
 gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163  
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala  
 10 15 20  
 tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211  
 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala  
 25 30 35  
 gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259  
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp  
 40 45 50  
 gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307  
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser  
 55 60 65  
 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355  
 Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys  
 70 75 80 85  
 ctg ttt tagtcttcat tcttgctggc tgc 384  
 Leu Phe



Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met  
 70 75 80 85  
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403  
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu  
 90 95 100  
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451  
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val  
 105 110 115  
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499  
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala  
 120 125 130  
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547  
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
 135 140 145  
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595  
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
 150 155 160 165  
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
 170 175 180  
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
 185 190 195  
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739  
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp  
 200 205 210  
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775  
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu  
 215 220 225

&lt;210&gt; 502

&lt;211&gt; 225

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 502

Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp  
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 Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly  
 20 25 30  
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser  
 35 40 45  
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
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 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80

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cgaactagcc cccaacaac aattagaaat ggaacctaaa atg cct gga aaa att 115
                                         Met Pro Gly Lys Ile
                                         1 5
ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
                        10                        15                        20
gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
                        25                        30                        35
gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
                        40                        45                        50
cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307

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His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
 55 60 65

atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355  
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg  
 70 75 80 85

ttt tgg atg ctg tgaaggcgctc tgagcttcct acc 390  
 Phe Trp Met Leu

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Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val  
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Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu  
 35 40 45

Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn  
 50 55 60

Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr  
 65 70 75 80

Thr Leu Arg Trp Arg Phe Trp Met Leu  
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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
 Met Thr Gln Ser Ala  
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
           40                          45                          50  
  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
           55                          60                          65  
  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
           70                          75                          80                          85  
  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                           90                          95                          100  
  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                           105                          110                          115  
  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130  
  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
  
 cag taatttgttt tgacgacgca gta 621  
 Gln

&lt;210&gt; 506

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 506

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
   1                          5                          10                          15  
  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                          25                          30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                          40                          45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
           85                          90                          95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160

Glu Ala Pro Ile Lys Gln  
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aacactgcc aacacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg 115  
 Val Leu Gly Ala Val  
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163  
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp  
 10 15 20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211  
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val  
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259  
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu  
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc -aac gtg gtc atg 307  
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met  
 55 60 65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355  
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly  
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403  
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys  
 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451  
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val  
 105 110 115

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
120 125 130	
gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc	547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt	883
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
250 255 260	
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg	931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac	979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
280 285 290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	
1027 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	
295 300 305	
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg	
1075 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	
310 315 320 325	
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc	
1123 Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile	
330 335 340	

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg  
 1171  
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu  
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac  
 1219  
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn  
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc  
 1267  
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg  
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg  
 1315  
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu  
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg  
 1363  
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu  
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta  
 1411  
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu  
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc  
 1459  
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe  
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc  
 1507  
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt  
 1555  
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
1747  
Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc  
1795  
His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala  
550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc  
1843  
Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala  
570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag  
1891  
Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
585 590 595

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1939  
Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg  
1987  
Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val  
615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt  
2035  
Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly  
630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc  
2083  
Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr  
650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag  
2131  
Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys  
665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg  
2179  
Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc  
2227  
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695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc  
2275  
Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc  
 2323  
 Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro  
                     730                    735                    740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc  
 2371  
 Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr  
                     745                    750                    755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct  
 2419  
 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro  
                     760                    765                    770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg  
 2467  
 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met  
                     775                    780                    785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc  
 2515  
 Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala  
                     790                    795                    800                    805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa  
 2563  
 Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln  
                     810                    815                    820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct  
 2611  
 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
                     825                    830                    835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat  
 2659  
 Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
                     840                    845                    850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc  
 2707  
 Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
                     855                    860                    865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc  
 2755  
 Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser  
                     870                    875                    880                    885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc  
 2803  
 Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser  
                     890                    895                    900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc  
 2851  
 Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala  
                     905                    910                    915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat  
2899  
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg  
2947  
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca  
2995  
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt  
3043  
Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac  
3075  
Val Gly Trp

<210> 508  
<211> 984  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 508  
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Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu  
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Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
35 40 45  
Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln  
50 55 60  
Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln  
65 70 75 80  
Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
85 90 95  
Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
100 105 110  
Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu  
115 120 125  
His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
130 135 140  
Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
 165 170 175  
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
 180 185 190  
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
 195 200 205  
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met  
 210 215 220  
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala  
 225 230 235 240  
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala  
 245 250 255  
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
 260 265 270  
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn  
 275 280 285  
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu  
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 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu  
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 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr  
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 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser  
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 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
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 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
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 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
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 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
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 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
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Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
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 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
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 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
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 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
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 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
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 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
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 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala  
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 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
 610 615 620  
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
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 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
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 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
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 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala  
 725 730 735  
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
 740 745 750  
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu  
 755 760 765  
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
 770 775 780  
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val  
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 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

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Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser
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Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr
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Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp
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Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp
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Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile
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 Met Ser Ile Glu Trp  
 1 5  
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 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala  
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 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro  
 25 30 35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
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act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
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tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
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Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
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Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
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Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
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Thr Val Ile Val Met Thr Ile Gly	
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 <212> PRT  
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<400> 510

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Leu	Val	Ser	Phe	Pro	Ile	Leu	Val	Phe	Leu	Gly	Leu	Pro	Pro	Leu	Thr
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Ala	Thr	Ile	Ala	Asn	Thr	Ile	Gly	Ile	Val	Pro	Gly	Ser	Ile	Ser	Gly
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Val	Val	Ala	Tyr	Arg	Arg	Glu	Leu	His	Ala	His	Val	Lys	Thr	Ile	Arg
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Phe	Leu	Leu	Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ile	Thr	Gly	Ala	Ser	Leu
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Leu	Leu	His	Phe	Ser	Ala	Asp	Val	Phe	Thr	Ala	Val	Ile	Pro	Trp	Leu
			100					105					110		
Ile	Gly	Phe	Gly	Thr	Leu	Leu	Val	Ile	Ala	Gly	Pro	Ser	Ile	Lys	Lys
		115					120					125			
His	Val	Gly	Ala	His	Thr	Ser	Gly	Gly	Ile	Ser	Ala	Gly	Phe	Arg	Gln
	130					135					140				
Leu	Pro	Phe	Pro	Ser	Arg	Thr	Thr	Phe	Ile	Val	Ser	Val	Cys	Gly	Ala
	145				150					155					160
Leu	Leu	Leu	Gly	Met	Tyr	Gly	Gly	Tyr	Phe	Ser	Ala	Ala	Gln	Gly	Ile
				165				170						175	
Leu	Leu	Ile	Ala	Leu	Leu	Gly	Ile	Thr	Ser	Thr	Leu	Gln	Met	Gln	Glu
			180					185					190		
Leu	Asn	Ala	Ile	Lys	Asn	Leu	Thr	Val	Ala	Ala	Val	Asn	Leu	Ile	Ala
		195					200					205			
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		210				215					220				
Val	Ala	Leu	Ile	Ala	Leu	Gly	Ser	Ala	Leu	Gly	Gly	Tyr	Ile	Gly	Gly
	225				230					235				240	
Arg	Tyr	Ala	Arg	Arg	Leu	Arg	Pro	Ser	Val	Phe	Arg	Ala	Phe	Val	Val
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<223> RXC02789

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Met Lys Val Ser Ala  
1 5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163  
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu  
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gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211  
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala  
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aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259  
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys  
40 45 50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307  
 Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu  
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tac	aac	gcc	gtg	gaa	gtc	att	gtt	ggc	cta	ccc	aca	gat	ctg	cag	gga	355
Tyr	Asn	Ala	Val	Glu	Val	Ile	Val	Gly	Leu	Pro	Thr	Asp	Leu	Gln	Gly	
70					75					80					85	

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403  
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val  
90 95 100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451  
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly  
105 110 115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499  
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser  
120 125 130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat-caa gct gcc gca 547  
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala  
135 140 145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595  
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu  
150 155 160 165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643  
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170 175 180

gga tgaaccaa at ccgaaaccgc cgg 669  
Gly

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                               Met Gly Leu Glu Leu
                               1               5
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atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	40 45 50	259
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	55 60 65	307
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	70 75 80 85	355
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	90 95 100	403
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	105 110 115	451
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	120 125 130	499
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	135 140 145	547
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	150 155 160 165	595
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	170 175 180	643
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	185 190 195	691
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	200 205 210	739
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	215 220 225	787
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	230 235 240 245	835

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<212> PRT

<213> Corynebacterium glutamicum

<400> 514

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                   20                  25                  30  
 Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val  
                   35                  40                  45  
 Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
                   50                  55                  60  
 Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
                   65                  70                  75                  80  
 Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
                   85                  90                  95  
 Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
                   100                  105                  110  
 Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
                   115                  120                  125  
 Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
                   130                  135                  140  
 Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
                   145                  150                  155                  160  
 Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
                   165                  170                  175  
 Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
                   180                  185                  190  
 Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
                   195                  200                  205  
 Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
                   210                  215                  220  
 Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
                   225                  230                  235                  240  
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<223> RXN03063

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Val Glu Asp Leu Ser 5  
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tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163  
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro 20  
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Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala 35  
25 30  
  
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Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile 50  
40 45  
  
ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307  
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile 65  
55 60  
  
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Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val 85  
70 75 80  
  
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403  
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro 100  
90 95  
  
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451  
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro 115  
105 110  
  
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499  
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala 130  
120 125  
  
gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547  
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala 145  
135 140  
  
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595  
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met 165  
150 155 160

gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643  
 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu  
 170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691  
 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly  
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ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739  
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 200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787  
 Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln  
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ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835  
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 230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883  
 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile  
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caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931  
 Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu  
 265 270 275

ggt gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979  
 Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly  
 280 285 290

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 295 300 305

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 310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag  
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 35 40 45  
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp  
 50 55 60  
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala  
 65 70 75 80  
 Val Ala Lys Ala Val Gly Ala Ala Ala Arg Phe Thr His Thr Cys  
 85 90 95  
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 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr  
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 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile  
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 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys  
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<223> RXN02970

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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
70 75 80 85  
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Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
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Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
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His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
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ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
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375 380 385	

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1315  
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425 430 435

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1459  
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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
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Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
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His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
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Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
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Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
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Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

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His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg
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Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu
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Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly
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225					230					235				Gly
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Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly
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Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp
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Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr
	290					295					300			Ala
Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe
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Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu
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Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu
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Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile
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Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp
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 <223> FRXA01009

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tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
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gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
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Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
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cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
                                   150                               155                               160                               165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
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acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

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His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala	
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atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro	
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Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile	
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Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys	
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1219																
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1267																
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Arg	Ala	His	Val	Phe	His	Ser	Trp	Ser	Ala	Gln	Asp	Lys	Ile	Ser	Pro	35	40	45	
Lys	Val	Trp	Ala	Ala	Ala	Glu	Gly	Ser	Thr	Leu	Tyr	Asp	Phe	Asp	Gly	50	55	60	
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Leu	Thr	Asn	Ile	Asn	Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	100	105	110	
Ala	Ala	Lys	Ile	Val	Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	115	120	125	
Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	130	135	140	
Arg	Leu	His	Thr	Gly	Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	145	150	155	160
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	165	170	175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	180	185	190	
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	195	200	205	
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	210	215	220	
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	225	230	235	240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	245	250	255	

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 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
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 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
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 <223> RXA01551

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 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala  
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 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly  
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 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser  
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Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu Thr Glu Ile Arg Leu  
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gat gac tcg cca agc ggc ccc aac gaa ccc ttc cgc atc tac cgc acc 355  
 Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe Arg Ile Tyr Arg Thr  
 70 75 80 85

cgt ggc cca gaa acc aac ccc aag cag gga ctt ccg cgg ctg cgc gag 403  
 Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu Pro Arg Leu Arg Glu  
 90 95 100

tca tgg atc acc gcc cgc ggc gac gtt gcc acc tat cag ggg cgc gag 451  
 Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr Tyr Gln Gly Arg Glu  
 105 110 115

cgt ttg ctt atc gac gac ggc cgc tcg gca atg cgt cga ggt caa gct 499  
 Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met Arg Arg Gly Gln Ala  
 120 125 130

tcg gct gag tgg aaa ggc caa aaa cca gct cct ttg aag gcg cta cct 547  
 Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro Leu Lys Ala Leu Pro  
 135 140 145

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 Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg Ala Gly Val Ile Thr  
 150 155 160 165

cgt gaa atg gag ttt gta gcg ctg cgc gaa cac gtt gat gcg gag ttt 643  
 Arg Glu Met Glu Phe Val Ala Leu Arg Glu His Val Asp Ala Glu Phe  
 170 175 180

gtg cgc tct gag gtg gcg cgc ggt cgg gcc att att ccc aac aac gtc 691  
 Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile Ile Pro Asn Asn Val  
 185 190 195

aac cac ccc gaa tct gaa ccg atg att att ggt cgc aaa ttt ttg acc 739  
 Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly Arg Lys Phe Leu Thr  
 200 205 210

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 Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val Thr Ser Ser Ile Glu  
 215 220 225

gaa gag gtg tcc aag ctg cag tgg gcc acg cgc tgg ggt gcc gat acc 835  
 Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg Trp Gly Ala Asp Thr  
 230 235 240 245

gtg atg gat cta tcc acc ggc gat gat att cac acc acc cgc gaa tgg 883  
 Val Met Asp Leu Ser Thr Gly Asp Asp Ile His Thr Thr Arg Glu Trp  
 250 255 260

att atc cgc aac tcc ccc gtt cct atc ggc acc gtc ccg atc tac caa 931  
 Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr Val Pro Ile Tyr Gln  
 265 270 275

gcg ctg gaa aaa gta aat ggc gtg gcc gca gac ctt aac tgg gaa gta 979  
 Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp Leu Asn Trp Glu Val  
 280 285 290

ttc cgc gat acc atc att gag cag tgt gaa caa ggc gtg gac tat atg  
 1027

Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met  
 295 300 305  
 acc atc cac gcc ggc gtc ctg ctg gct tat atc cca ctg act acc cgt  
 1075  
 Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg  
 310 315 320 325  
 cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg  
 1123  
 Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp  
 330 335 340  
 tgt ctg gcg cat cac cgc gaa tca ttc ctc tac gag cat ttc gac gag  
 1171  
 Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu  
 345 350 355  
 ctg tgc gaa atc ttt gca caa tat gac gtc gca ttc tcc ctc ggt gat  
 1219  
 Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp  
 360 365 370  
 ggc cta cgc ccc gga tcg ctt gcc gat gcc aac gac gcc gcg caa ttc  
 1267  
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe  
 375 380 385  
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac  
 1315  
 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr  
 390 395 400 405  
 gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg  
 1363  
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met  
 410 415 420  
 atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct  
 1411  
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro  
 425 430 435  
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac  
 1459  
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp  
 440 445 450  
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc  
 1507  
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr  
 455 460 465  
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac  
 1555  
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn  
 470 475 480 485  
 cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac  
 1603  
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

490 495 500  
 gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac  
 1651  
 Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp  
 505 510 515  
 gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg  
 1699  
 Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala  
 520 525 530  
 ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg  
 1747  
 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu  
 535 540 545  
 ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg  
 1795  
 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro  
 550 555 560 565  
 aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc  
 1843  
 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly  
 570 575 580  
 gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt  
 1891  
 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser  
 585 590 595  
 gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg  
 1939  
 Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg  
 600 605 610  
 gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc  
 1985  
 Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg Arg  
 615 620 625  
 gatcccagat agc  
 1998

&lt;210&gt; 522

&lt;211&gt; 625

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 522

Leu Lys Ala Val Pro Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu  
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 Ile Ala Ala Arg Ala Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys  
 20 25 30  
 Glu Glu Arg Asn Gly Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro  
 35 40 45

Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu  
 50 55 60  
 Thr Glu Ile Arg Leu Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe  
 65 70 75 80  
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu  
 85 90 95  
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr  
 100 105 110  
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met  
 115 120 125  
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro  
 130 135 140  
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg  
 145 150 155 160  
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His  
 165 170 175  
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile  
 180 185 190  
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly  
 195 200 205  
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val  
 210 215 220  
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg  
 225 230 235 240  
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His  
 245 250 255  
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr  
 260 265 270  
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp  
 275 280 285  
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln  
 290 295 300  
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile  
 305 310 315 320  
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser  
 325 330 335  
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr  
 340 345 350  
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala  
 355 360 365  
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370	375	380
Asp 385	Ala 390	Glu 395
Ala	Leu	Lys
Gln	Thr	Ile
Phe	Gly	Glu
Ala	Leu	Thr
Gln	Gln	400
Arg	Ala	Trp
Glu	Tyr	Asp
Val	Val	Gln
Val	Met	Val
Glu	Gly	Pro
Gly	Gly	His
Pro	Gly	415
Val	Pro	Leu
Asn	Met	Ile
Gln	Gln	Glu
Asn	Asn	Glu
Leu	Glu	Gln
Lys	Trp	420
Ala	Ala	Asp
Ala	Pro	Phe
Tyr	Thr	Leu
Thr	Gly	Pro
Leu	Val	Thr
Asp	Ile	435
Ala	Pro	Gly
Tyr	Asp	His
His	Ile	Thr
Thr	Ser	Ala
Ile	Gly	Ile
Gly	Ala	Ala
His	Ile	440
Ala	Met	Gly
Gly	Gly	Thr
Thr	Ala	Met
Leu	Cys	Tyr
Val	Thr	Pro
Lys	Glu	His
His	465	480
Leu	Gly	Leu
Pro	Asn	Arg
Asp	Asp	Val
Lys	Thr	Gly
Val	Ile	Thr
Tyr	485	495
Lys	Leu	Ala
Ala	His	Ala
Ala	Ala	Asp
Val	Ala	Lys
Gly	His	Pro
Gly	Ala	500
Arg	Ala	Trp
Asp	Asp	Ala
Met	Ser	Lys
Ala	Arg	Phe
Glu	Phe	Arg
Trp	515	525
Asn	Asp	Gln
Phe	Ala	Leu
Ser	Leu	Asp
Pro	Asp	Thr
Ala	Ile	Ala
Tyr	530	540
His	Asp	Glu
Thr	Leu	Pro
Ala	Glu	Pro
Ala	Lys	Thr
Ala	His	Phe
Cys	545	560
Ser	Met	Cys
Gly	Pro	Lys
Phe	Cys	Ser
Met	Arg	Ile
Ser	Gln	Asp
Ile	565	575
Arg	Asp	Met
Phe	Gly	Asp
Gln	Ile	Ala
Glu	Leu	Gly
Met	Pro	Gly
Val	580	590
Gly	Asp	Ser
Ser	Ser	Ala
Val	Ala	Ser
Ser	Ser	Gly
Ala	Arg	Glu
Gly	Met	595
Ala	Glu	Lys
Ser	Arg	Glu
Phe	Ile	Ala
Gly	Gly	Ala
Glu	Val	Tyr
Arg	610	620
Arg	625	

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (1)..(990)  
 <223> RXA01019

&lt;400&gt; 523

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Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro	
1 5 10 15	
acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag	96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu	
20 25 30	
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat	144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His	
35 40 45	
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg	192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala	
50 55 60	
ggg agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag	240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln	
65 70 75 80	
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt	288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	
85 90 95	
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg	336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	
100 105 110	
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag	384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	
115 120 125	
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg	432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	
130 135 140	
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag	480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	
145 150 155 160	
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga	528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	
165 170 175	
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt	576
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	
180 185 190	
cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc	624
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	
195 200 205	
gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga	672
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	
210 215 220	
gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac	720
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	
225 230 235 240	

caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
                   245                                  250                                  255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
                   260                                  265                                  270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
                   275                                  280                                  285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
                   290                                  295                                  300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
                   305                                  310                                  315                                  320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg  
 1010  
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
                   325                                  330

aat  
 1013

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 524  
 Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro  
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 Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
                   20                                  25                                  30  
 Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
                   35                                  40                                  45  
 Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
                   50                                  55                                  60  
 Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
   65                                  70                                  75                                  80  
 Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg  
                   85                                  90                                  95  
 Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
                   100                                  105                                  110  
 Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu  
                   115                                  120                                  125  
 Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
                   130                                  135                                  140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
145 150 155 160

Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
165 170 175

Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
180 185 190

Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
195 200 205

Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
210 215 220

Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
225 230 235 240

Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
245 250 255

Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
260 265 270

Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
275 280 285

Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
290 295 300

Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
305 310 315 320

Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
325 330

<210> 525

<211> 706

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXA01352

<400> 525

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ctggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115  
Val Phe Glu Asn Arg  
1 5

ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163  
Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu  
10 15 20

gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211  
Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

	25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca				259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala				
	40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg				307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val				
	55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga				355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly				
	70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt				403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu				
	90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act				451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr				
	105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg				499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu				
	120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca				547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser				
	135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg				595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu				
	150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg				643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val				
	170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct				691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala				
	185	190	195	
ttt tct gaa tct gat				706
Phe Ser Glu Ser Asp				
	200			

&lt;210&gt; 526

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

Val	Phe	Glu	Asn	Arg	Phe	Asp	Leu	Arg	Cys	Tyr	Val	Val	Thr	Gly	Ala
1				5					10					15	

Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
		20					25					30			

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
	35					40					45				

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser  
 50 55 60  
 Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser  
 65 70 75 80  
 Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp  
 85 90 95  
 Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile  
 100 105 110  
 Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu  
 115 120 125  
 Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr  
 130 135 140  
 Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro  
 145 150 155 160  
 Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val  
 165 170 175  
 Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val  
 180 185 190  
 Ala Met Val Arg Ala Phe Ser Glu Ser Asp  
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 att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt 96  
 Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
 20 25 30  
 cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca 144  
 Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
 35 40 45  
 gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc 192  
 Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
 50 55 60  
 tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct 240  
 Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser

65	70					75					80					
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act	Phe Ser Thr Lys Tyr 85					Ala Ala Glu Ile Thr 95					Gly Thr					288
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc	Pro Leu Ile Trp Ala Thr Val Leu 100					Phe His Gly Glu Leu 110					Ala Leu					336
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc	Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu 115					Arg Gly Val Gly Leu 125					Asp Val Phe					384
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt	Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly 130					135					140					432
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac	Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His 145					150					155					480
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc	Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile 165					170					175					528
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc	Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser 180					185					190					576
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag	Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu 195					200					205					624
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc	Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly 210					215					220					672
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa	Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys 225					230					235					720
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc	Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile 245					250					255					768
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac	Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp 260					265					270					816
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac	Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp 275					280					285					864
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc	Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val 290					295					300					912
aac gcg ctg tagctgtcaa tttaagaggc cag	Asn Ala Leu															944
305																

&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp  
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Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
 20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
 35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
 50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser  
 65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr  
 85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu  
 100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe  
 115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly  
 130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His  
 145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile  
 165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser  
 180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu  
 195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly  
 210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys  
 225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile  
 245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp  
 260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp  
 275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val  
 290 295 300

Asn Ala Leu  
 305

<210> 529  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(259)  
 <223> RXA01360

<400> 529  
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 gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115  
 Met Leu His Ile Ala  
 1 5  
 gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163  
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr  
 10 15 20  
 tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211  
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu  
 25 30 35  
 acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259  
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu  
 40 45 50

<210> 530  
 <211> 53  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 530  
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly  
 1 5 10 15  
 Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala  
 20 25 30  
 Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr  
 35 40 45  
 Thr Ser Ser Gly Glu  
 50

<210> 531  
 <211> 629  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(606)

&lt;223&gt; RXA01361

&lt;400&gt; 531

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gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg      48
Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
  1                      5                      10                      15

acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg      96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
                20                      25                      30

gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg      144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
                35                      40                      45

aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc      192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
                50                      55                      60

gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt      240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
  65                      70                      75                      80

gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc      288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
                85                      90                      95

gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc      336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
                100                      105                      110

gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att      384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
                115                      120                      125

gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc      432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
                130                      135                      140

ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg      480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
  145                      150                      155                      160

tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca      528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
                165                      170                      175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt      576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
                180                      185                      190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga      626
Asp Val Cys Asp Pro Phe Arg His Gln Ile
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tta                                                                 629

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 <211> 202  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 532  
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 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu  
           20                  25                  30  
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala  
       35                  40                  45  
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg  
       50                  55                  60  
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe  
   65                  70                  75                  80  
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu  
           85                  90                  95  
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly  
          100                 105                 110  
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile  
      115                 120                 125  
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr  
   130                 135                 140  
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala  
 145                 150                 155                 160  
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
          165                 170                 175  
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
      180                 185                 190  
 Asp Val Cys Asp Pro Phe Arg His Gln Ile  
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<210> 533  
 <211> 927  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(904)  
 <223> RXA01208

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 aacctgctct agctcgctact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

	Val	Ala	Asn	Ser	Phe	
	1				5	
ttg gat tct tta act ctt gtt cga caa aac act ccc ctt gtt cag tgt						163
Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr Pro Leu Val Gln Cys						
	10		15		20	
ttg acc aac tct gtg gtc atg caa ttc acg gcc aat gtg ttg ctt gcc						211
Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala Asn Val Leu Leu Ala						
	25		30		35	
gcg ggt gcg acc cct gcg atg gtg gat act cca gct gaa tcg gca gaa						259
Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro Ala Glu Ser Ala Glu						
	40		45		50	
ttc gcc gct gtg gcc aat gga gtg ctc atc aat gcg gga act cct tct						307
Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn Ala Gly Thr Pro Ser						
	55		60		65	
gcg gag caa tac caa ggc atg acc aag gcc att gag ggt gca cga aaa						355
Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile Glu Gly Ala Arg Lys						
	70		75		80	85
gct ggc aca cca tgg gtg tta gac cca gtt gct gtg ggt ggg ttg tcg						403
Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala Val Gly Gly Leu Ser						
	90		95		100	
gag agg acc aag tat gcg gag gga atc gtc gat aag cag cct gcc gca						451
Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp Lys Gln Pro Ala Ala						
	105		110		115	
att cgt gga aac gcc tca gag gtc gtg gcg ctt gcg ggg ctc ggt gcc						499
Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu Ala Gly Leu Gly Ala						
	120		125		130	
ggt ggg cgc ggc gta gac gcg acc gat tcc gtg gaa gtg gcg ttg gag						547
Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val Glu Val Ala Leu Glu						
	135		140		145	
gcg gcg caa ttg ttg gcc aag cgc act ggt ggc gtc gtg gct gtc tct						595
Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly Val Val Ala Val Ser						
	150		155		160	165
ggt gcg gag gac ttg att gtg tct gcg gat cgg gtg acg tgg ttg cgt						643
Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg Val Thr Trp Leu Arg						
	170		175		180	
tcg ggg gat ccg atg ttg cag ctg gtg att ggc act gga tgc tct ttg						691
Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly Thr Gly Cys Ser Leu						
	185		190		195	
ggc gcg ctg aca gct gca tat cta ggc gcc acg gtt gac tca gat att						739
Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr Val Asp Ser Asp Ile						
	200		205		210	
tcc gcg cac gat gct gtg ttg gct gcg cat gcc cat gtg ggt gct gct						787
Ser Ala His Asp Ala Val Leu Ala Ala His Ala His Val Gly Ala Ala						
	215		220		225	
ggc cag att gca gca cag aag gca tcg gcg cca ggc agc ttt gcg gtg						835
Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro Gly Ser Phe Ala Val						

230                                      235                                      240                                      245

gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg      883  
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser  
    250                                      255                                      260

ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt      927  
 Leu Val Asp Val Arg Glu Ala  
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<210> 534

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 534

Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr  
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Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala  
    20                                      25                                      30

Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro  
    35                                      40                                      45

Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn  
    50                                      55                                      60

Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile  
     65                                      70                                      75                                      80

Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala  
    85                                      90                                      95

Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp  
    100                                      105                                      110

Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu  
    115                                      120                                      125

Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val  
    130                                      135                                      140

Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly  
     145                                      150                                      155                                      160

Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg  
    165                                      170                                      175

Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly  
    180                                      185                                      190

Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr  
    195                                      200                                      205

Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala  
    210                                      215                                      220

His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro  
     225                                      230                                      235                                      240

Gly Ser Phe Ala Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala  
 245 250 255

Gln Ala Val Ala Ser Leu Val Asp Val Arg Glu Ala  
 260 265

<210> 535

<211> 1023

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1000)

<223> RXA00838

<400> 535

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tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115  
 Met Lys Ile Ala Ile  
 1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu  
 10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211  
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala  
 25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259  
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr  
 40 45 50

gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307  
 Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp  
 55 60 65

gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct 355  
 Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala  
 70 75 80 85

gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403  
 Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln  
 90 95 100

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451  
 Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp  
 105 110 115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499  
 Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro  
 120 125 130

gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547  
 Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp  
 135 140 145

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595  
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly  
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643  
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys  
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691  
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys  
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739  
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu  
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787  
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro  
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835  
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu  
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883  
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser  
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931  
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val  
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979  
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu  
 280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg  
 1023  
 Lys Glu Glu Glu Asn Ser Leu  
 295 300

<210> 536

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly  
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Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly  
 20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala  
 35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
 50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

65		70		75		80									
Ser	Leu	Asp	Leu	Ala	Glu	Leu	Leu	Gly	Gly	Ile	Pro	Ala	Asn	Ser	Val
				85					90					95	
Val	Ala	Ile	Thr	Gln	Asn	Ser	Ile	Glu	Ser	Ala	Asp	Leu	Ala	Ala	Lys
			100					105					110		
Ser	Ile	Gly	Ala	Asp	Arg	Val	Trp	Pro	Gly	Val	Val	Arg	Gly	Phe	Phe
		115					120					125			
Val	His	Glu	Gly	Pro	Ala	Ser	Val	Ser	Tyr	Lys	Gly	Gly	Pro	Leu	Ser
	130					135					140				
Tyr	Thr	Phe	Gly	Asp	Ser	Gly	Glu	Leu	Ser	Arg	Gln	Phe	Ala	Ser	Thr
145					150					155					160
Leu	Glu	Gln	Ala	Gly	Ile	Asp	Gly	Val	Leu	His	Pro	Asp	Ile	Leu	Val
				165					170					175	
Asp	Val	Trp	Glu	Lys	Ala	Met	Phe	Val	Glu	Val	Phe	Gly	Gly	Leu	Gly
			180					185					190		
Ala	Phe	Val	Glu	Lys	Gln	Leu	Gly	Thr	Leu	Arg	Thr	His	Phe	Arg	Ala
		195					200					205			
Ser	Leu	Glu	Ala	Leu	Met	Glu	Glu	Val	Ala	Glu	Val	Ala	Arg	Ala	Ala
	210					215					220				
Gly	Val	Ala	Leu	Pro	Ser	Asp	Ala	Val	Glu	Arg	Thr	Met	Asn	Phe	Ala
225					230					235					240
Asp	Arg	Met	Pro	Glu	Asn	Ser	Thr	Ser	Ser	Met	Gln	Arg	Asp	Leu	Ala
				245					250					255	
Ala	Gly	Val	Ala	Ser	Glu	Leu	Glu	Ala	Gln	Thr	Gly	Ala	Ile	Val	Arg
			260					265					270		
Ala	Ala	His	Lys	Val	Gly	Val	Lys	Thr	Pro	Leu	His	Asp	Leu	Ile	Tyr
		275					280					285			
Ala	Gly	Leu	Lys	Leu	Lys	Glu	Glu	Glu	Asn	Ser	Leu				
	290					295					300				

&lt;210&gt; 537

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02400

&lt;400&gt; 537

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tttaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115  
 Met Ser Ile Ser Arg  
 1 5

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163  
 Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val  
 10 15 20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211  
 Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn  
 25 30 35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259  
 Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser  
 40 45 50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307  
 Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val  
 55 60 65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355  
 Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr  
 70 75 80 85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403  
 Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile  
 90 95 100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451  
 Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly  
 105 110 115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499  
 Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro  
 120 125 130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547  
 Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu  
 135 140 145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595  
 Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys  
 150 155 160 165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643  
 Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala  
 170 175 180

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 Glu Val Pro Val Thr Phe Ala Ala Ala  
 185 190

tca 693

<210> 538  
 <211> 190  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 538  
 Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu  
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Ser Ala Ala Leu Val Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro  
 20 25 30  
 Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser  
 35 40 45  
 Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro  
 50 55 60  
 Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp  
 65 70 75 80  
 Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly  
 85 90 95  
 Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val  
 100 105 110  
 Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu  
 115 120 125  
 Ser Asn Ser Gln Pro Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr  
 130 135 140  
 Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys  
 145 150 155 160  
 Thr Thr Gln Ala Cys Val Ala Lys Val Phe Gly Asp His Thr Glu Gly  
 165 170 175  
 Phe Arg Asp Val Ala Glu Val Pro Val Thr Phe Ala Ala Ala  
 180 185 190

<210> 539  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1528)  
 <223> RXN01209

<400> 539  
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 Met Cys Glu Arg Pro  
 1 5  
 gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20  
 ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
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&lt;210&gt; 540

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 540

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Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
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 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350  
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365  
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380  
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400  
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415  
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
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Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
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Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
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Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
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Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
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Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
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Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
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Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
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Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
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Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
260 265 270

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 Asp Asn Lys  
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&lt;210&gt; 544

&lt;211&gt; 200

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&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 544

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Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
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gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
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Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
	135	140	145
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Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
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Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
	170	175	180
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
	185	190	195
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
	200	205	210
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Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
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Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala			
1	5	10	15
Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu			
20	25	30	

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
 35 40 45  
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
 50 55 60  
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
 65 70 75 80  
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr  
 85 90 95  
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu  
 100 105 110  
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly  
 115 120 125  
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn  
 130 135 140  
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu  
 145 150 155 160  
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala  
 165 170 175  
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala  
 180 185 190  
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val  
 195 200 205  
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
 210 215 220

&lt;210&gt; 547

&lt;211&gt; 638

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(615)

&lt;223&gt; FRXA01617

&lt;400&gt; 547

gct aat cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg 48  
 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
 1 5 10 15  
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96  
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
 20 25 30  
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144  
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala 50 55 60			192
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn 65 70 75 80			240
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp 85 90 95			288
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr 100 105 110			336
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp 115 120 125			384
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile 130 135 140			432
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile 145 150 155 160			480
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr 165 170 175			528
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn 180 185 190			576
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatcctt Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys 195 200 205			625
aaacaagctc cct			638
<210> 548			
<211> 205			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 548			
Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val 1 5 10 15			
Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr 20 25 30			
Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu 35 40 45			
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			

50	55	60
Leu Arg Ala Lys Val	Leu Pro Gln Ala Thr	Val Val Thr Pro Asn Asn
65	70	75 80
Phe Glu Ala Thr Thr	Leu Ser Gly Leu Asp	Lys Leu Glu Thr Ile Asp
	85	90 95
Asp Leu Lys Glu Ala Ala	Arg Leu Ile His Glu Gln Gly	Pro Gln Tyr
	100	105 110
Val Val Val Lys Gly Gly	Ile Asp Phe Pro Gly Asp	Asn Ala Val Asp
	115	120 125
Val Leu Phe Asp Gly Thr	Asp Tyr His Val Phe Ser	Glu Pro Lys Ile
	130	135 140
Gly Asp Glu Arg Val Ser	Gly Ala Gly Cys Thr Phe	Ala Ala Val Ile
	145	150 155 160
Thr Ala Glu Leu Ala Lys	Gly Asn Ser Ala Val Asp	Ala Val Thr Thr
	165	170 175
Ala Lys Arg Val Val Thr	Arg Ala Val Lys Asp	Ala Val Ala Ser Asn
	180	185 190
Ala Pro Phe Thr Ser Val	Trp Leu Ala Glu Asp	Asn Lys
	195	200 205

<210> 549  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXS01807

<400> 549  
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 Met Pro Ser Ala Gly  
 1 5  
 gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163  
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg  
 10 15 20  
 gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211  
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly  
 25 30 35  
 ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259  
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val  
 40 45 50  
 gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307  
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp 70 75 80 85			355
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly 90 95 100			403
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln 105 110 115			451
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile 120 125 130			499
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr 135 140 145			547
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn 150 155 160 165			595
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu 170 175 180			643
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr 185 190 195			691
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu 200 205 210			739
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val 215 220 225			787
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile 230 235 240 245			835
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr 250 255 260			883
aaa gcg ctt taggtttcgt ccgtctctga cag Lys Ala Leu			915

&lt;210&gt; 550

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 550

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu  
 1 5 10 15  
 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val  
 20 25 30  
 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu  
 35 40 45  
 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro  
 50 55 60  
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala  
 65 70 75 80  
 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser  
 85 90 95  
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val  
 100 105 110  
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile  
 115 120 125  
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala  
 130 135 140  
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr  
 145 150 155 160  
 Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly  
 165 170 175  
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr  
 180 185 190  
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg  
 195 200 205  
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys  
 210 215 220  
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys  
 225 230 235 240  
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys  
 245 250 255  
 Ala Gly Leu Gln Thr Lys Ala Leu  
 260

<210> 551  
 <211> 622  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(622)  
 <223> RXC01021

&lt;400&gt; 551

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gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115  
 Met Ser Ser Ser Glu  
 1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163  
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu  
 10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211  
 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala  
 25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259  
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala  
 40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307  
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val  
 55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355  
 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met  
 70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403  
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val  
 90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451  
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg  
 105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499  
 Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln  
 120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547  
 Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu  
 135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595  
 Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu  
 150 155 160 165

ggc act gtt gtc act gtg ttg cgt tct 622  
 Gly Thr Val Val Thr Val Leu Arg Ser  
 170

&lt;210&gt; 552

&lt;211&gt; 174

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 552

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro  
 1 5 10 15

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<400> 553
tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60
caacaaggcg atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac 115
Met Asp Val Ala His
1 5
gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
10 15 20
agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
25 30 35
gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
40 45 50

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gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg	307
Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala	
55 60 65	
gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt	355
Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys	
70 75 80 85	
tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc  
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr  
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga  
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg  
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga  
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
 210 215 220  
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
 225 230 235 240  
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
 245 250 255  
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
 260 265 270  
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
 275 280 285  
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
 290 295 300  
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
 305 310 315 320  
 Ile Glu Met Met Arg Lys Glu His  
 325

<210> 555  
 <211> 1107  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1084)  
 <223> FRXA02246

<400> 555  
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 caacaaggcg atccaggagt tgcgagcact cgcgacagtaa atg gat gtt gcg cac 115  
 Met Asp Val Ala His  
 1 5  
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163  
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
 10 15 20  
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211  
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu  
 25 30 35  
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259  
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu  
 40 45 50  
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307  
 Val Val Ala Leu Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala  
 55 60 65  
 gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355  
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys  
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat 403  
 Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn  
 90 95 100

gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag 451  
 Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu  
 105 110 115

gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag 499  
 Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu  
 120 125 130

ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag 547  
 Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys  
 135 140 145

ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc 595  
 Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser  
 150 155 160 165

cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga 643  
 Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg  
 170 175 180

agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat 691  
 Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp  
 185 190 195

aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa 739  
 Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln  
 200 205 210

ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac 787  
 Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn  
 215 220 225

ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta 835  
 Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu  
 230 235 240 245

tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc 883  
 Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly  
 250 255 260

cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg 931  
 Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val  
 265 270 275

cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att 979  
 Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile  
 280 285 290

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc  
 1027  
 Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr  
 295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga  
 1075  
 Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga  
 1107  
 Lys Glu His

&lt;210&gt; 556

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 556

Met	Asp	Val	Ala	His	Ala	Leu	Asp	Leu	Ala	His	His	Val	Ser	Asp	Gln
1				5					10					15	
Val	Arg	Gly	Thr	Thr	Ser	Pro	Asn	Pro	Pro	Val	Gly	Ala	Val	Ile	Leu
			20					25					30		
Asp	Ala	Asp	Gly	Glu	Val	Val	Gly	Val	Gly	Ala	Thr	Ala	Pro	Pro	Gly
		35					40					45			
Gly	Pro	His	Ala	Glu	Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala
	50					55					60				
Asn	Gly	Gly	Thr	Ala	Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly
65					70					75				80	
Arg	Thr	Gly	Pro	Cys	Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His
				85					90					95	
Val	Phe	Tyr	Ala	Asn	Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly
			100					105					110		
Ala	Phe	Leu	Ala	Glu	Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg
		115					120					125			
Ile	Arg	Ala	Leu	Glu	Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro
	130					135					140				
His	Val	Thr	Leu	Lys	Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala
145					150					155				160	
Thr	Asp	Gly	Thr	Ser	Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe
				165					170					175	
Val	His	Glu	Asp	Arg	Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly
			180					185					190		
Thr	Ala	Leu	Thr	Asp	Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly
		195				200						205			
Leu	Tyr	Glu	Asn	Gln	Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val
	210					215					220				
Pro	Ala	Asp	Ser	Asn	Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly
225					230					235				240	
Ile	Pro	Glu	Ala	Leu	Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile
			245						250					255	

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
                   260                                  265                                  270  
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
                   275                                  280                                  285  
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
                   290                                  295                                  300  
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
                   305                                  310                                  315                                  320  
 Ile Glu Met Met Arg Lys Glu His  
                                   325

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   Met Phe Thr Gly Ile  
   1  5  
 gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163  
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser  
                                   10                                  15                                  20  
 atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211  
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu  
                                   25                                  30                                  35  
 ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259  
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe  
                                   40                                  45                                  50  
 ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307  
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg  
                                   55                                  60                                  65  
 agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355  
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg  
                                   70                                  75                                  80                                  85  
 gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403  
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His  
                                   90                                  95                                  100  
 gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451  
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp  
                                   105                                  110                                  115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499  
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val  
120 125 130  
  
gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547  
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser  
135 140 145  
  
ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595  
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg  
150 155 160 165  
  
gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643  
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu  
170 175 180  
  
gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691  
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
185 190 195  
  
gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733  
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp  
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taggttagac aacgtgagtg aac 756

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Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu  
35 40 45  
Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln  
50 55 60  
Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys  
65 70 75 80  
Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His  
85 90 95  
Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr  
100 105 110  
Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu  
115 120 125  
Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser  
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile  
145 150 155 160

Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp  
165 170 175

Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met  
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Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe  
195 200 205

Thr Arg Asp  
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<210> 559

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1366)

<223> RXN02248

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aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115  
Val Ser Glu His Glu  
1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163  
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile  
10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211  
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn  
25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val  
40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307  
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr  
55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355  
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn  
70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403  
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr  
90 95 100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451  
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499  
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His  
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547  
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly  
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595  
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro  
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643  
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met  
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691  
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys  
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739  
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile  
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787  
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr  
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835  
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val  
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883  
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu  
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931  
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg  
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979  
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln  
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga  
 1027  
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg  
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa  
 1075  
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu  
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat  
 1123  
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp  
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg  
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val  
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt  
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu  
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct  
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala  
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg  
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met  
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa  
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu  
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1389

Asn

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<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

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Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
 145 150 155 160  
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
 165 170 175  
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
 180 185 190  
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
 195 200 205  
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
 210 215 220  
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
 225 230 235 240  
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
 245 250 255  
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
 420

&lt;210&gt; 561

&lt;211&gt; 1389

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

804

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 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787  
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr  
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835  
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val  
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883  
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu  
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931  
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg  
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979  
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln  
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga  
 1027  
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg  
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa  
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 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu  
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat  
 1123  
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp  
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg  
 1171  
 Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val  
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt  
 1219  
 Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu  
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct  
 1267  
 Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala  
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg  
 1315  
 Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met  
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa  
 1363  
 Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu



Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
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 <213> Corynebacterium glutamicum

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 <223> RXN02249

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 Met Ala Lys Glu Gly  
 1 5  
 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
 10 15 20  
 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
 25 30 35  
 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu  
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597  
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
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ttg 600

<210> 564  
<211> 159  
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<400> 564  
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20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr  
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala  
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

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<223> FRXA02249

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 Met Ala Lys Glu Gly  
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259  
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
 40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
 55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
 70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
 90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
 105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
 Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
 120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145

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ttg 600

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 <213> Corynebacterium glutamicum

<400> 566  
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 20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr  
 35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
 50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
 65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
 85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
 100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly  
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala  
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
 145 150 155

<210> 567  
 <211> 702  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(679)  
 <223> RXA02250

<400> 567  
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tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115  
 Val Thr Thr Asn Ala

811

**Asp**

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gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
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ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

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cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly 70 75 80 85			355
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu 90 95 100			403
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala 105 110 115			451
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ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn 135 140 145			547
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acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn 170 175 180			643
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly 185 190 195			691
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr 200 205 210			739
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp 215 220 225			787
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp 230 235 240 245			835
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser 250 255 260			883
gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala 265 270 275			931

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979  
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val  
           280                                  285                                  290

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 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp  
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gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc  
 1075  
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile  
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ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct  
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                                   20                                  25                                  30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro  
                                   35                                  40                                  45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro  
                                   50                                  55                                  60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu  
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Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys  
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Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val  
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Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe  
                                   115                                  120                                  125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln  
                                   130                                  135                                  140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp  
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Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu

165										170					175															
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Glu	Val	Val	Arg	Gly	Ala	Gly	Arg	Gly	Gly	Lys	Glu	Leu	Gly	Tyr	Pro															
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Thr	Ala	Asn	Leu	Tyr	Leu	Pro	Thr	Ser	Val	Ala	Leu	Pro	Ala	Asp	Gly															
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Val	Tyr	Ala	Gly	Trp	Phe	Thr	Ile	Thr	Asp	Asp	Arg	Glu	Ile	Asp	Lys															
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Glu	Ile	Ser	Arg	Asp	Ile	Asp	Gly	Thr	Met	Val	Pro	Gly	Val	Arg	Tyr															
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Gln	Thr	Ala	Ile	Ser	Val	Gly	Thr	Asn	Pro	Thr	Phe	Gly	Asp	Glu	Arg															
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Arg	Ser	Val	Glu	Ala	Phe	Ile	Leu	Asp	Gln	Glu	Ala	Asp	Leu	Tyr	Gly															
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His	His	Val	Met	Val	Glu	Phe	Val	Gly	His	Leu	Arg	Asp	Met	Val	Lys															
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Phe	Asn	Gly	Val	Asp	Glu	Leu	Leu	Asp	Ala	Met	Ala	Arg	Asp	Val	Thr															
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Asn	Ala	Arg	Asp	Ile	Leu	Ala	Lys	Asp	Lys	Leu	Leu	Leu	Asp	Ala	Asp															
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 Met Val Pro Ala Glu  
 1 5  
 ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163  
 Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr  
 10 15 20  
 aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211  
 Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys  
 25 30 35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
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ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser  
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gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg  
 1027

Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met  
 295 300 305

tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag  
 1075

Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys  
 310 315 320 325

att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc  
 1123

Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly  
 330 335 340

gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg  
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<213> Corynebacterium glutamicum

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 35 40 45

Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val  
 50 55 60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro  
 65 70 75 80

Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala  
 85 90 95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile  
 100 105 110

Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg  
 115 120 125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val  
 130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp  
 145 150 155 160  
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr  
 165 170 175  
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val  
 180 185 190  
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu  
 195 200 205  
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg  
 210 215 220  
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala  
 225 230 235 240  
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val  
 245 250 255  
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys  
 260 265 270  
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr  
 275 280 285  
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile  
 290 295 300  
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala  
 305 310 315 320  
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr  
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 Pro Glu Gln Asn Thr Glu  
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 Val Asp Ile Trp Ser  
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gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
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Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883

Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser  
 250 255 260

gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca 931  
 Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala  
 265 270 275

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979  
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val  
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac  
 1027  
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp  
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc  
 1075  
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile  
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct  
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 330 335 340

taaggccggt caccggccat caa  
 1146

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 <213> Corynebacterium glutamicum

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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln  
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Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro  
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro  
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu  
 65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys  
 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val  
 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe  
 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln

130 135 140  
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp  
 145 150 155 160  
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu  
 165 170 175  
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly  
 180 185 190  
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro  
 195 200 205  
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly  
 210 215 220  
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys  
 225 230 235 240  
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr  
 245 250 255  
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg  
 260 265 270  
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly  
 275 280 285  
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys  
 290 295 300  
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr  
 305 310 315 320  
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp  
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 Thr Gln Pro Ser Ala  
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 <223> RXN01712

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 Met Val Asp Ile Leu Glu Leu Ile Gly  
 1 5  
 ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161  
 Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

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gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga				209
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile	110	115	120	
acg gat aat tcc gat caa gca aag cag cag cgg ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His	170	175	180	185
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys	220	225	230	
tgagtgttgg actctccgga tct				805

&lt;210&gt; 576

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 576

Met Val Asp Ile Leu Glu Leu Ile Gly Pro Leu Pro Phe Val Ser Thr  
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Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr  
 20 25 30

Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu  
 35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser  
 50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile  
 65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala  
 85 90 95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu  
 100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala  
 115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu  
 130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr  
 145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu  
 165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu  
 180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro  
 195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu  
 210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys  
 225 230

&lt;210&gt; 577

&lt;211&gt; 578

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (55) .. (555)

&lt;223&gt; FRXA01712

&lt;400&gt; 577

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 Val

1

aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105  
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys  
5 10 15  
  
caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153  
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met  
20 25 30  
  
tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201  
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala  
35 40 45  
  
gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249  
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln  
50 55 60 65  
  
cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297  
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu  
70 75 80  
  
acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345  
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg  
85 90 95  
  
att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393  
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala  
100 105 110  
  
gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441  
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly  
115 120 125  
  
agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489  
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg  
130 135 140 145  
  
ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537  
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu  
150 155 160  
  
cgg tat aag cgc gcc aag tgagtgttgg actctccgga tct 578  
Arg Tyr Lys Arg Ala Lys  
165

&lt;210&gt; 578

&lt;211&gt; 167

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 578

Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln  
1 5 10 15  
  
Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val  
20 25 30  
  
Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu  
35 40 45

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys  
 50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr  
 65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala  
 85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala  
 100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser  
 115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg  
 130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe  
 145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys  
 165

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 <213> Corynebacterium glutamicum

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 Val Thr Arg Arg Leu  
 1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163  
 Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met  
 10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211  
 Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala  
 25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259  
 Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe  
 40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307  
 Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala  
 55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355  
 Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaa atg				831
Trp Asn Met Gly Val Thr Gln	230	235		

&lt;210&gt; 580

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 580

Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn			
1	5	10	15

Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu			
20	25	30	

Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn			
35	40	45	

Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala			
50	55	60	

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg  
 65 70 75 80  
 Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu  
 85 90 95  
 Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro  
 100 105 110  
 Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg  
 115 120 125  
 Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp  
 130 135 140  
 Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu  
 145 150 155 160  
 Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser  
 165 170 175  
 Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr  
 180 185 190  
 Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala  
 195 200 205  
 Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln  
 210 215 220  
 Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln  
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 Val Gly Val Ser Tyr  
 1 5  
 atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163  
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys  
 10 15 20  
 att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211  
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly  
 25 30 35  
 acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259  
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40	45	50	
atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg			307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu			
55	60	65	
ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca			355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser			
70	75	80	85
ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac			403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr			
90	95	100	
ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc			450
Gly Val Asn Gly Pro Val Asp Ala Asn			
105	110		
ttt			453
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<211> 110			
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Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala			
1	5	10	15
Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile			
20	25	30	
Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu			
35	40	45	
Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys			
50	55	60	
His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu			
65	70	75	80
Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser			
85	90	95	
Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn			
100	105	110	
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829

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835  
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu  
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883  
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg  
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931  
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu  
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979  
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu  
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg  
 1027  
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met  
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag  
 1075  
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu  
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt  
 1124  
 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu  
 330 335

agacatcacc cag  
 1137

<210> 584

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 584

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Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val  
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu  
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu  
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly  
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp  
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His  
 100 105 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr  
 115 120 125  
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val  
 130 135 140  
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg  
 145 150 155 160  
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu  
 165 170 175  
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys  
 180 185 190  
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly  
 195 200 205  
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln  
 210 215 220  
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser  
 225 230 235 240  
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His  
 245 250 255  
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly  
 260 265 270  
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile  
 275 280 285  
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp  
 290 295 300  
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp  
 305 310 315 320  
 Pro Gln Thr Asn Glu Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly  
 325 330 335

Ser Leu

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 <212> DNA  
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 <223> RXC01711

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																Met	Leu	Leu	Met	Ala	
																1				5	
cat	cgc	ttc	ttc	gtg	ctt	gcg	att	aac	ggc	gca	gtc	acc	gac	gat	ttc	163					
His	Arg	Phe	Phe	Val	Leu	Ala	Ile	Asn	Gly	Ala	Val	Thr	Asp	Asp	Phe						
				10					15					20							
acg	acg	gtt	tat	agt	gct	tta	cga	cgt	ttc	gtt	gaa	ggg	att	ccg	gtc	211					
Thr	Thr	Val	Tyr	Ser	Ala	Leu	Arg	Arg	Phe	Val	Glu	Gly	Ile	Pro	Val						
				25					30					35							
tac	aac	gag	gtc	tac	cac	ttc	gtc	gat	ccg	cac	tac	ctc	tat	aac	ccg	259					
Tyr	Asn	Glu	Val	Tyr	His	Phe	Val	Asp	Pro	His	Tyr	Leu	Tyr	Asn	Pro						
				40					45					50							
ggc	gcc	acc	ctc	cta	ttg	gca	cca	ttg	gga	tat	atc	acc	cat	ttc	acg	307					
Gly	Ala	Thr	Leu	Leu	Leu	Ala	Pro	Leu	Gly	Tyr	Ile	Thr	His	Phe	Thr						
				55					60					65							
ttg	gct	cgg	tgg	atg	ttc	atc	gcg	gtg	aac	ctc	ctt	gcc	att	gtt	tta	355					
Leu	Ala	Arg	Trp	Met	Phe	Ile	Ala	Val	Asn	Leu	Leu	Ala	Ile	Val	Leu						
				70					75					80							
gcg	ttc	ggg	ctg	ctg	acc	aga	ctc	tcc	ggg	tgg	gcg	ctg	cgc	agc	atg	403					
Ala	Phe	Gly	Leu	Leu	Thr	Arg	Leu	Ser	Gly	Trp	Ala	Leu	Arg	Ser	Met						
				90					95					100							
gtg	tgg	ccg	att	gcg	atc	gcc	ttg	gcg	atg	ctg	aca	gaa	acc	gtg	caa	451					
Val	Trp	Pro	Ile	Ala	Ile	Ala	Leu	Ala	Met	Leu	Thr	Glu	Thr	Val	Gln						
				105					110					115							
aac	acc	ctc	att	ttc	tcc	aac	atc	aac	ggc	atc	ctg	ctg	ctc	atg	ttg	499					
Asn	Thr	Leu	Ile	Phe	Ser	Asn	Ile	Asn	Gly	Ile	Leu	Leu	Leu	Met	Leu						
				120					125					130							
gcg	att	ttc	ctg	tgg	tgc	gtg	gtg	cac	aaa	aaa	tcc	tgg	ttg	ggc	gga	547					
Ala	Ile	Phe	Leu	Trp	Cys	Val	Val	His	Lys	Lys	Ser	Trp	Leu	Gly	Gly						
				135					140					145							
cta	gtc	att	ggg	ttg	gcc	att	ttg	atc	aaa	ccc	atg	ttc	ctg	cca	ctt	595					
Leu	Val	Ile	Gly	Leu	Ala	Ile	Leu	Ile	Lys	Pro	Met	Phe	Leu	Pro	Leu						
				150					155					160							
ctc	ttc	cta	cct	ttg	gtg	aaa	aag	caa	tgg	gga	tcg	ctc	atc	ctc	ggc	643					
Leu	Phe	Leu	Pro	Leu	Val	Lys	Lys	Gln	Trp	Gly	Ser	Leu	Ile	Leu	Gly						
				170					175					180							
att	tta	acc	cca	gtg	att	ttc	aat	gca	gtg	gcc	tgg	ttc	tta	gtt	ccg	691					
Ile	Leu	Thr	Pro	Val	Ile	Phe	Asn	Ala	Val	Ala	Trp	Phe	Leu	Val	Pro						
				185					190					195							
gga	gca	tct	gaa	tac	gtc	acc	cgc	acg	atg	ccc	tac	ctt	ggg	gaa	act	739					
Gly	Ala	Ser	Glu	Tyr	Val	Thr	Arg	Thr	Met	Pro	Tyr	Leu	Gly	Glu	Thr						
				200					205					210							
cga	gat	ttt	gcc	aac	agc	tca	ctc	cca	ggc	ttg	gcc	atc	tat	ttc	gga	787					
Arg	Asp	Phe	Ala	Asn	Ser	Ser	Leu	Pro	Gly	Leu	Ala	Ile	Tyr	Phe	Gly						
				215					220					225							
atg	ccc	acc	tgg	atg	gaa	atc	acc	tgg	ttc	ctc	atc	ttc	ggc	gca	atg	835					
Met	Pro	Thr	Trp	Met	Glu	Ile	Thr	Trp	Phe	Leu	Ile	Phe	Gly	Ala	Met						

230                      235                      240                      245  
 gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca 883  
 Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro  
                          250                      255                      260  
 tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc 931  
 Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe  
                          265                      270                      275  
 ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct 979  
 Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro  
                          280                      285                      290  
 atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt  
 1027  
 Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val  
                          295                      300                      305  
 gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc  
 1075  
 Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser  
 310                      315                      320                      325  
 cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc  
 1123  
 Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr  
                          330                      335                      340  
 gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc  
 1171  
 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile  
                          345                      350                      355  
 tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att  
 1219  
 Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile  
                          360                      365                      370  
 acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt  
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 Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala  
                          375                      380                      385  
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 1281

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 <211> 386  
 <212> PRT  
 <213> Corynebacterium glutamicum

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 Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val  
                           20                          25                          30  
 Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His

35	40	45
Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr		
50	55	60
Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu		
65	70	75 80
Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp		
	85	90 95
Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu		
	100	105 110
Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile		
	115	120 125
Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys		
	130	135 140
Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro		
145	150	155 160
Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly		
	165	170 175
Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala		
	180	185 190
Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro		
	195	200 205
Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu		
210	215	220
Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu		
225	230	235 240
Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe		
	245	250 255
Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu		
	260	265 270
Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser		
	275	280 285
Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val		
290	295	300
Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro		
305	310	315 320
Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu		
	325	330 335
Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe		
	340	345 350
Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr		
	355	360 365

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg  
 370 375 380

Thr Ala  
 385

<210> 587  
 <211> 777  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101) .. (754)  
 <223> RXC02380

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 Met Thr Thr Thr Val  
 1 5  
 aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163  
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile  
 10 15 20  
 cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211  
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp  
 25 30 35  
 ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259  
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala  
 40 45 50  
 aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307  
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile  
 55 60 65  
 gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355  
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp  
 70 75 80 85  
 cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403  
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys  
 90 95 100  
 caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451  
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu  
 105 110 115  
 gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499  
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala  
 120 125 130  
 cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547  
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile  
 135 140 145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595  
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala  
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643  
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg  
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691  
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739  
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys  
 200 205 210

ggc caa aac caa gca taaatctagt caaaagtttc aac 777  
 Gly Gln Asn Gln Ala  
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<210> 588

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 588

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Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val  
 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln  
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser  
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys  
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu  
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu  
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg  
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

180	185	190
Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys		
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Asp Met Asp Pro Lys Gly Gln Asn Gln Ala		
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	Met Thr Thr Thr Val	
	1 5	
aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163		
Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile		
10	15	20
cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211		
His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp		
25	30	35
ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259		
Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala		
40	45	50
aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307		
Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile		
55	60	65
gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355		
Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp		
70	75	80 85
cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403		
Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys		
90	95	100
caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451		
Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu		
105	110	115
gca cag atc gtg acg tgg gcg gat tgg gag aaa acc ttc gaa ctt gcc 499		
Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala		
120	125	130
cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547		
His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile		
135	140	145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595  
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala  
 150 155 160 165  
  
 atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643  
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg  
 170 175 180  
  
 cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691  
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys  
 185 190 195  
  
 cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739  
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys  
 200 205 210  
  
 ggc caa aac caa gca taaatctagt caaaagtttc aac 777  
 Gly Gln Asn Gln Ala  
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&lt;210&gt; 590

&lt;211&gt; 218

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 590

Met Thr Thr Thr Val Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly  
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 Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val  
 20 25 30  
  
 Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln  
 35 40 45  
  
 Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr  
 50 55 60  
  
 Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser  
 65 70 75 80  
  
 Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu  
 85 90 95  
  
 Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr  
 100 105 110  
  
 Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys  
 115 120 125  
  
 Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu  
 130 135 140  
  
 Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu  
 145 150 155 160  
  
 Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg  
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val  
 180 185 190

Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys  
 195 200 205

Asp Met Asp Pro Lys Gly Gln Asn Gln Ala  
 210 215

<210> 591

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (571)

<223> RXC02921

<400> 591

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aaaagggtga ggaaccacat gagctgtttt aaggaatttt gtg tct gca ctt gaa 115  
 Val Ser Ala Leu Glu  
 1 5

gag tcg atc cgc atc gcg acc atc gcg gcg aaa gca gcg gat gaa aag 163  
 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys  
 10 15 20

aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211  
 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile  
 25 30 35

acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259  
 Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly  
 40 45 50

gcc att gtt gag gag atc gaa gat gag atg acc aag gct ggt ttc gag 307  
 Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu  
 55 60 65

cct aag cgc cgt gaa ggc aac cgc gaa aac cgt tgg gtt ctc ctt gac 355  
 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp  
 70 75 80 85

tac gga ttg gtt gtt atc cac gtt cag cga cag gca gag cgc gag ttc 403  
 Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe  
 90 95 100

tac gga ctg gat cgt ctg tac cgc gac tgc cca ctc att gaa att gaa 451  
 Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu  
 105 110 115

gga ctt gaa acc ttc aag cgt gaa tcc tcc tgg tct gat gag gcg gat 499  
 Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp  
 120 125 130

atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa 547  
 Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

135 140 145  
 tac gag cct ggc tac gag gac gat taagaggtag tcctgtgact cgt 594  
 Tyr Glu Pro Gly Tyr Glu Asp Asp  
 150 155

<210> 592  
 <211> 157  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 592  
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 Asp Met Ile Ala Ile Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn  
 35 40 45  
 Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr  
 50 55 60  
 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg  
 65 70 75 80  
 Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln  
 85 90 95  
 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro  
 100 105 110  
 Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp  
 115 120 125  
 Ser Asp Glu Ala Asp Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro  
 130 135 140  
 Pro Leu Pro Ala Glu Tyr Glu Pro Gly Tyr Glu Asp Asp  
 145 150 155

<210> 593  
 <211> 3075  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101) .. (3052)  
 <223> RXC01434

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 aacactgcca acacgctgcc caacctgatc actggaaatc gtg ttg ggt gcg gtg 115  
 Val Leu Gly Ala Val  
 1 5

ctg	aca	tcg	ctg	gtt	att	ccg	gtc	ctt	acc	cgc	gcg	gaa	aaa	gaa	gac	163
Leu	Thr	Ser	Leu	Val	Ile	Pro	Val	Leu	Thr	Arg	Ala	Glu	Lys	Glu	Asp	
				10					15					20		
gcc	gac	ggc	ggg	tcc	ggg	ttc	ttc	agg	cgg	ctg	ctc	acc	ctg	tcg	gtg	211
Ala	Asp	Gly	Gly	Ser	Gly	Phe	Phe	Arg	Arg	Leu	Leu	Thr	Leu	Ser	Val	
			25					30					35			
acg	ctg	ctg	ggg	ggg	gtc	acc	atc	ctg	tcg	att	atc	ggc	gcg	ccg	ctg	259
Thr	Leu	Leu	Gly	Gly	Val	Thr	Ile	Leu	Ser	Ile	Ile	Gly	Ala	Pro	Leu	
			40				45					50				
ctg	aca	cgg	atg	atg	ctg	tcc	tct	gag	gga	caa	gtc	aac	gtg	gtc	atg	307
Leu	Thr	Arg	Met	Met	Leu	Ser	Ser	Glu	Gly	Gln	Val	Asn	Val	Val	Met	
	55					60					65					
tcc	acg	gcc	ttt	gcg	tat	tgg	ctg	ctg	cca	cag	att	ttc	ttc	tac	ggc	355
Ser	Thr	Ala	Phe	Ala	Tyr	Trp	Leu	Leu	Pro	Gln	Ile	Phe	Phe	Tyr	Gly	
	70				75					80					85	
ctg	ttt	gcc	ctg	ttc	atg	gct	gtg	ttg	aac	acc	cgt	gaa	gtg	ttc	aaa	403
Leu	Phe	Ala	Leu	Phe	Met	Ala	Val	Leu	Asn	Thr	Arg	Glu	Val	Phe	Lys	
				90					95					100		
ccc	ggc	gcg	tgg	gca	cct	gtt	gtc	aac	aat	gtg	atc	acc	ttg	acc	gtg	451
Pro	Gly	Ala	Trp	Ala	Pro	Val	Val	Asn	Asn	Val	Ile	Thr	Leu	Thr	Val	
			105					110					115			
ctg	ggc	gtg	tac	atg	gtg	ctg	cct	gcg	cgt	ttg	cac	ccg	cat	gag	cag	499
Leu	Gly	Val	Tyr	Met	Val	Leu	Pro	Ala	Arg	Leu	His	Pro	His	Glu	Gln	
		120					125					130				
gtg	ggc	att	ttt	gat	ccg	cag	atc	att	ttc	ctc	ggc	gtg	ggc	acc	acc	547
Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu	Gly	Val	Gly	Thr	Thr	
	135					140					145					
ctt	ggg	gtg	gtt	gca	cag	tgt	cta	atc	atg	att	ccg	tac	ctg	cgt	cgc	595
Leu	Gly	Val	Val	Ala	Gln	Cys	Leu	Ile	Met	Ile	Pro	Tyr	Leu	Arg	Arg	
					155					160					165	
gcg	ggc	att	gat	atg	cgc	cct	ctg	tgg	ggg	atc	gat	gcg	cgt	ttg	aag	643
Ala	Gly	Ile	Asp	Met	Arg	Pro	Leu	Trp	Gly	Ile	Asp	Ala	Arg	Leu	Lys	
				170					175					180		
caa	ttc	ggg	ggc	atg	gcg	atg	gcg	atc	atc	gtg	tac	gtg	gca	atc	tcc	691
Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val	Tyr	Val	Ala	Ile	Ser	
			185					190					195			
cag	ttc	ggg	tac	atc	atc	acc	act	cgc	att	gcg	tcg	att	gca	gac	gat	739
Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala	Ser	Ile	Ala	Asp	Asp	
		200					205					210				
gct	gcg	ccg	ttt	att	tat	cag	cag	cac	tgg	atg	ttg	ctg	caa	gtt	cct	787
Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met	Leu	Leu	Gln	Val	Pro	
		215				220					225					
tat	ggc	atc	atc	ggc	gtc	acc	ttg	ctc	acc	gcg	att	atg	ccg	cga	ctg	835
Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala	Ile	Met	Pro	Arg	Leu	
	230				235					240					245	
tcc	cgc	aac	gcg	gca	gac	ggc	gat	gat	agg	gca	gta	gtc	tct	gac	ctt	883

Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala	Val	Val	Ser	Asp	Leu	
				250					255					260		
cag	ttg	ggt	tcc	aag	cta	acc	ttc	atc	gca	ctg	atc	ccc	atc	gtg	gtg	931
Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu	Ile	Pro	Ile	Val	Val	
			265					270					275			
ttc	ttc	acc	gcc	ttc	ggt	gtc	cct	att	gcc	aat	ggc	ctt	ttt	gcc	tac	979
Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn	Gly	Leu	Phe	Ala	Tyr	
		280					285					290				
ggc	caa	ttc	gat	gcc	aac	gcc	gcc	aac	atc	ctt	ggt	tgg	act	ctg	agc	
1027																
Gly	Gln	Phe	Asp	Ala	Asn	Ala	Ala	Asn	Ile	Leu	Gly	Trp	Thr	Leu	Ser	
	295					300					305					
ttc	tct	gct	ttc	acg	ctg	att	cct	tac	gct	ttg	gtg	ctg	cta	cat	ctg	
1075																
Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu	Val	Leu	Leu	His	Leu	
310					315					320					325	
cgt	gtg	ttt	tat	gcg	cgt	gaa	gag	gtc	tgg	acc	cca	acc	ttc	atc	atc	
1123																
Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr	Pro	Thr	Phe	Ile	Ile	
				330					335					340		
gcc	ggc	atc	acc	gcc	acc	aag	gtc	gtg	ctt	tcc	ctg	ttg	gca	ccg	ctg	
1171																
Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser	Leu	Leu	Ala	Pro	Leu	
			345					350					355			
ctg	tcg	agc	tcc	ccg	gag	cgt	gtg	gtg	gtg	ctt	ctt	ggt	gcg	gcc	aac	
1219																
Leu	Ser	Ser	Ser	Pro	Glu	Arg	Val	Val	Val	Leu	Leu	Gly	Ala	Ala	Asn	
		360					365					370				
ggt	ttc	agt	ttc	atc	acc	ggc	gcg	gtc	atc	ggc	gcg	tat	ctg	ttg	cgc	
1267																
Gly	Phe	Ser	Phe	Ile	Thr	Gly	Ala	Val	Ile	Gly	Ala	Tyr	Leu	Leu	Arg	
	375					380					385					
aac	aaa	ctc	ggc	ctg	ttg	ggt	atg	cgc	tct	ttg	gct	aaa	acc	tcc	ctg	
1315																
Asn	Lys	Leu	Gly	Leu	Leu	Gly	Met	Arg	Ser	Leu	Ala	Lys	Thr	Ser	Leu	
390					395					400					405	
tgg	gcg	ttg	ggc	tct	gcg	gcg	gtt	ggt	gca	gca	gca	gca	tgg	gcg	ttg	
1363																
Trp	Ala	Leu	Gly	Ser	Ala	Ala	Val	Gly	Ala	Ala	Ala	Ala	Trp	Ala	Leu	
				410					415					420		
ggg	tgg	ctg	att	caa	gcc	gtc	gtg	ggc	gat	ttc	ttg	ctg	ggc	act	cta	
1411																
Gly	Trp	Leu	Ile	Gln	Ala	Val	Val	Gly	Asp	Phe	Leu	Leu	Gly	Thr	Leu	
			425					430					435			
agc	tcc	gta	ggc	tac	ttg	ttg	aac	ctg	gct	gtg	ttg	ggt	gtc	ttc	ttc	
1459																
Ser	Ser	Val	Gly	Tyr	Leu	Leu	Asn	Leu	Ala	Val	Leu	Gly	Val	Phe	Phe	
		440					445					450				

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc  
 1507  
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt  
 1555  
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
 1747  
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc  
 1795  
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala  
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc  
 1843  
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala  
 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag  
 1891  
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta  
 1939  
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg  
 1987  
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val  
 615 620 625

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 630 635 640 645

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 2131  
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys  
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 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
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 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
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aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc  
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 2419  
 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro  
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gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg  
 2467  
 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met  
                     775                    780                    785

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 Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln  
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 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
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Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
840 845 850

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Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
855 860 865

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2755  
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser  
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc  
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890 895 900

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920 925 930

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2947  
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
935 940 945

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2995  
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
950 955 960 965

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Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
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Val	Asn	Val	Val	Met	Ser	Thr	Ala	Phe	Ala	Tyr	Trp	Leu	Leu	Pro	Gln
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Ile	Phe	Phe	Tyr	Gly	Leu	Phe	Ala	Leu	Phe	Met	Ala	Val	Leu	Asn	Thr
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Arg	Glu	Val	Phe	Lys	Pro	Gly	Ala	Trp	Ala	Pro	Val	Val	Asn	Asn	Val
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Ile	Thr	Leu	Thr	Val	Leu	Gly	Val	Tyr	Met	Val	Leu	Pro	Ala	Arg	Leu
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His	Pro	His	Glu	Gln	Val	Gly	Ile	Phe	Asp	Pro	Gln	Ile	Ile	Phe	Leu
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Gly	Val	Gly	Thr	Thr	Leu	Gly	Val	Val	Ala	Gln	Cys	Leu	Ile	Met	Ile
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Pro	Tyr	Leu	Arg	Arg	Ala	Gly	Ile	Asp	Met	Arg	Pro	Leu	Trp	Gly	Ile
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Asp	Ala	Arg	Leu	Lys	Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val
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Tyr	Val	Ala	Ile	Ser	Gln	Phe	Gly	Tyr	Ile	Ile	Thr	Thr	Arg	Ile	Ala
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Ser	Ile	Ala	Asp	Asp	Ala	Ala	Pro	Phe	Ile	Tyr	Gln	Gln	His	Trp	Met
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Leu	Leu	Gln	Val	Pro	Tyr	Gly	Ile	Ile	Gly	Val	Thr	Leu	Leu	Thr	Ala
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Ile	Met	Pro	Arg	Leu	Ser	Arg	Asn	Ala	Ala	Asp	Gly	Asp	Asp	Arg	Ala
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Val	Val	Ser	Asp	Leu	Gln	Leu	Gly	Ser	Lys	Leu	Thr	Phe	Ile	Ala	Leu
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Ile	Pro	Ile	Val	Val	Phe	Phe	Thr	Ala	Phe	Gly	Val	Pro	Ile	Ala	Asn
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	290					295					300				
Gly	Trp	Thr	Leu	Ser	Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu
	305			310							315			320	
Val	Leu	Leu	His	Leu	Arg	Val	Phe	Tyr	Ala	Arg	Glu	Glu	Val	Trp	Thr
			325					330					335		
Pro	Thr	Phe	Ile	Ile	Ala	Gly	Ile	Thr	Ala	Thr	Lys	Val	Val	Leu	Ser
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 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
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 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
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 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
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 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
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 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
 660 665 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
 675 680 685  
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
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 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
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 850 855 860  
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu  
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 885 890 895  
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr  
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 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile  
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 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp  
 930 935 940  
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp  
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gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211															
Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly 25 30 35															
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Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln 105 110 115															
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Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn 150 155 160 165															
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Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu 170 175 180															

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 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val  
 215 220 225  
 tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835  
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile  
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 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883  
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&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 596

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 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu  
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 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro  
 50 55 60  
 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala  
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 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser  
 85 90 95  
 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val  
 100 105 110  
 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile  
 115 120 125  
 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala  
 130 135 140  
 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr  
 145 150 155 160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly  
 165 170 175  
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr  
 180 185 190  
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg  
 195 200 205  
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys  
 210 215 220  
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys  
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 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp  
 70 75 80 85  
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 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

852

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1123  
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330 335 340

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1219  
Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
360 365 370

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1267  
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375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
1315  
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390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta  
1363  
Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act  
1411  
Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr  
425 430 435

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Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu  
35 40 45  
Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu  
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu  
 65 70 75 80  
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe  
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 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln  
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 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125  
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160  
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175  
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 180 185 190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220  
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240  
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255  
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu  
 260 265 270  
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr  
 275 280 285  
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu  
 290 295 300  
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr  
 305 310 315 320  
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val  
 325 330 335  
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly  
 340 345 350  
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile  
 355 360 365  
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys  
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile  
385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys  
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Val Asn Thr Asn Pro  
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Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
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gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211  
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Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg  
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Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp  
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Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp  
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cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403  
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90 95 100

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Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr  
105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499  
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu  
120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca	871
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro	
250 255	

&lt;210&gt; 600

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 600

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu	
1 5 10 15	
Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp	
20 25 30	
Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu	
35 40 45	
Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu	
50 55 60	
Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu	
65 70 75 80	
Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe	
85 90 95	
Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln	
100 105 110	

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu  
 115 120 125  
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser  
 130 135 140  
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu  
 145 150 155 160  
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg  
 165 170 175  
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala  
 180 185 190  
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr  
 195 200 205  
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe  
 210 215 220  
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp  
 225 230 235 240  
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly  
 245 250 255

Pro

<210> 601  
 <211> 509  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(486)  
 <223> FRXA02754

<400> 601  
 ccc aca aac acc aag att gtg gtc tcc tcc gac ctg gat gaa ttc gcc 48  
 Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala  
 1 5 10 15  
 atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96  
 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr  
 20 25 30  
 tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144  
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys  
 35 40 45  
 atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192  
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys  
 50 55 60  
 gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240  
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser  
 65 70 75 80

ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288  
 Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro  
                     85                    90                    95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336  
 Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg  
                     100                    105                    110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384  
 Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala  
                     115                    120                    125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432  
 Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu  
                     130                    135                    140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480  
 Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro  
 145                    150                    155                    160

gcc gct tagacaattc ggtctcacca aac 509  
 Ala Ala

&lt;210&gt; 602

&lt;211&gt; 162

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 602

Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala  
 1                    5                    10                    15

Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr  
                     20                    25                    30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys  
                     35                    40                    45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys  
                     50                    55                    60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser  
 65                    70                    75                    80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro  
                     85                    90                    95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg  
                     100                    105                    110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala  
                     115                    120                    125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu  
                     130                    135                    140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro  
 145                    150                    155                    160

Ala Ala

<210> 603  
 <211> 960  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(937)  
 <223> RXA02112

<400> 603  
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agctcctggt actcctagct cctcgaagga tgcgtaattt atg act acc cat att 115  
 Met Thr Thr His Ile  
 1 5

gac cgc atc gtt ggc gca gcg tta tcc gag gat gcg cca tgg ggc gac 163  
 Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp Ala Pro Trp Gly Asp  
 10 15 20

att acc tcc gac act ttt atc cca gga tcg gcg cag ctg agc gcc aag 211  
 Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys  
 25 30 35

gtt gtt gcc cgg gag cca ggt gtg ttc agc ggg cag gcg ctt tta gac 259  
 Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Leu Asp  
 40 45 50

gcc tcc ttc cgg ctc gtc gat cct agg ata aac gca tcc ctt aag gtg 307  
 Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val  
 55 60 65

gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355  
 Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile Leu Gly Thr Ile Thr  
 70 75 80 85

ggc agt gct aga agc atc ctc cgt tca gag cgc att gct ctc aac ttc 403  
 Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg Ile Ala Leu Asn Phe  
 90 95 100

att cag agg acg tcc ggc atc gct aca ttg aca tcg tgc tat gtt gca 451  
 Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr Ser Cys Tyr Val Ala  
 105 110 115

gag gtt aaa ggc acc aaa gcc cgc att gtt gat acc cgg aaa acc aca 499  
 Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp Thr Arg Lys Thr Thr  
 120 125 130

ccc ggc ctg cgc atc att gaa cgc caa gct gtc cgt gac ggt ggc gga 547  
 Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly Gly  
 135 140 145

ttt aat cac cga gcc acc ttg tcc gat gct gtc atg gtg aaa gat aac 595  
 Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn  
 150 155 160 165

cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643  
 His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu  
 170 175 180  
 tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691  
 Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu  
 185 190 195  
 gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739  
 Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp  
 200 205 210  
 acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787  
 Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val  
 215 220 225  
 gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835  
 Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn  
 230 235 240 245  
 ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883  
 Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser  
 250 255 260  
 gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931  
 Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp  
 265 270 275  
 att ttc taatgctcta ccttgataat gca 960  
 Ile Phe

&lt;210&gt; 604

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 604

Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp  
 1 5 10 15  
 Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala  
 20 25 30  
 Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly  
 35 40 45  
 Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn  
 50 55 60  
 Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile  
 65 70 75 80  
 Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg  
 85 90 95  
 Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr  
 100 105 110

Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp  
 115 120 125  
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val  
 130 135 140  
 Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val  
 145 150 155 160  
 Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser  
 165 170 175  
 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr  
 180 185 190  
 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu  
 195 200 205  
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln  
 210 215 220  
 Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala  
 225 230 235 240  
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly  
 245 250 255  
 Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu  
 260 265 270  
 Asp Leu Gly Leu Asp Ile Phe  
 275

<210> 605  
 <211> 1407  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1384)  
 <223> RXA02111

<400> 605  
 gcttgcgga acaccgcacc gccaccccaa actgttcaga ttccaaagat aaattctgac 60  
 gctcattcca gccaccggt tagaagaaaa gaccccaatc atg acc acc tca atc 115  
 Met Thr Thr Ser Ile  
 1 5  
 acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163  
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser  
 10 15 20  
 gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211  
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp  
 25 30 35  
 gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259  
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

40	45	50	
ccg cgc cag cag gtt ctc ccc gag gag tac cag cgc gca agt gat gac Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp 55 60 65			307
gaa ctg cat cgt agg atc cgg gaa gcg aaa gac acc ctg ggt gac aaa Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys 70 75 80 85			355
gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His 90 95 100			403
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr 105 110 115			451
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala 120 125 130			499
gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro 135 140 145			547
aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser 150 155 160 165			595
gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr 170 175 180			643
ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe 185 190 195			691
gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser 200 205 210			739
gta ttg gag tgg gcg ttt gaa cgc ggc caa cga gtc ctg ttc ttc ccc Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro 215 220 225			787
gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile 230 235 240 245			835
gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr 250 255 260			883
gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys 265 270 275			931
tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala 280 285 290			979

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca  
 1027  
 Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro  
 295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa  
 1075  
 Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys  
 310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa  
 1123  
 Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu  
 330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc  
 1171  
 Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile  
 345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att  
 1219  
 Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile  
 360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac  
 1267  
 His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn  
 375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga  
 1315  
 Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg  
 390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act  
 1363  
 Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr  
 410 415 420

cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga  
 1407  
 Pro Ser Ser Ser Lys Asp Ala  
 425

<210> 606

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 606

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala  
 1 5 10 15

Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln  
 20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro  
 35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln  
 50 55 60  
 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp  
 65 70 75 80  
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp  
 85 90 95  
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala  
 100 105 110  
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly  
 115 120 125  
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln  
 130 135 140  
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met  
 145 150 155 160  
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile  
 165 170 175  
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala  
 180 185 190  
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser  
 195 200 205  
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg  
 210 215 220  
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala  
 225 230 235 240  
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro  
 245 250 255  
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu  
 260 265 270  
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile  
 275 280 285  
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro  
 290 295 300  
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr  
 305 310 315 320  
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe  
 325 330 335  
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr  
 340 345 350  
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser  
 355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu  
370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val  
385 390 395 400

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro  
405 410 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala  
420 425

<210> 607

<211> 954

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(931)

<223> RXA01073

<400> 607

taaccgactc cagcactaaa ctccaaaccc ttggcccgca ccgccaaagt ttagcgcgcc 60

ccaagacacc accgcgccat gtttgcctag gattaggtac atg aca aac act caa 115  
Met Thr Asn Thr Gln  
1 5

acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163  
Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala  
10 15 20

aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211  
Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala  
25 30 35

tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259  
Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser  
40 45 50

act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307  
Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala  
55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355  
Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr  
70 75 80 85

gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403  
Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile  
90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451  
Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala  
105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499  
Thr Glu Ala Thr Val Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp  
120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547  
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr  
 135 140 145  
  
 gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595  
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala  
 150 155 160 165  
  
 gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643  
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala  
 170 175 180  
  
 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691  
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile  
 185 190 195  
  
 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739  
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr  
 200 205 210  
  
 gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787  
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu  
 215 220 225  
  
 ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835  
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp  
 230 235 240 245  
  
 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883  
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly  
 250 255 260  
  
 cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931  
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg  
 265 270 275  
  
 taatccaaca gtttgagtgt cgc 954

&lt;210&gt; 608

&lt;211&gt; 277

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 608

Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro  
 1 5 10 15  
  
 Ala Ile Asp Val Ala Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val  
 20 25 30  
  
 Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser  
 35 40 45  
  
 Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val  
 50 55 60  
  
 Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala  
 65 70 75 80

Val Arg Leu Pro Tyr Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val  
85 90 95

Ala Leu Glu Phe Ile Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys  
100 105 110

Asp Ala Thr Asp Ala Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu  
115 120 125

Pro Glu Leu Thr Asp Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg  
130 135 140

Met Val Ala Gln Tyr Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile  
145 150 155 160

Gly Thr Asp His Ala Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe  
165 170 175

Gly Asp Gly Ala Ala Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg  
180 185 190

Gln Gly Ala Ala Ile Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp  
195 200 205

Thr Lys Val Pro Thr Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro  
210 215 220

Asp Glu Glu Ala Leu Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu  
225 230 235 240

Glu Asn Lys Pro Asp Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His  
245 250 255

Leu Trp Lys Val Gly Gln His Lys Arg His Leu Pro Ala Thr Pro Gln  
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Glu Asn Trp Trp Arg  
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<210> 609

<211> 1461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1438)

<223> RXN02754

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Val Asn Thr Asn Pro  
1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163  
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr  
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gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc	211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg	
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ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga	259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg	
40 45 50	
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Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp	
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Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp	
70 75 80 85	
cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat	403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp	
90 95 100	
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr	
105 110 115	
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu	
120 125 130	
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Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
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Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
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caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly	
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gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg  
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 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser  
 280 285 290  
 tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt  
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 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val  
 295 300 305  
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 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro  
 310 315 320 325  
 acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg  
 1123  
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val  
 330 335 340  
 gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct  
 1171  
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala  
 345 350 355  
 gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac  
 1219  
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr  
 360 365 370  
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 1267  
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser  
 375 380 385  
 ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct  
 1315  
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro  
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 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu  
 410 415 420  
 cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act  
 1411  
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr  
 425 430 435  
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 <213> Corynebacterium glutamicum

<400> 610

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			20					25					30		
Gly	Ser	Ala	Glu	Arg	Pro	Ser	Thr	Phe	Glu	Val	Phe	Ser	Arg	Arg	Leu
		35					40					45			
Pro	Asn	Glu	Arg	Arg	Tyr	Gly	Val	Val	Ala	Gly	Thr	Ala	Arg	Val	Leu
	50					55					60				
Lys	Ala	Ile	Arg	Asp	Phe	Val	Phe	Thr	Glu	Glu	Gln	Leu	Ala	Asp	Leu
65					70					75					80
Asp	Phe	Leu	Asp	Asp	Arg	Thr	Leu	Glu	Tyr	Leu	Arg	Asn	Tyr	Arg	Phe
				85					90					95	
Thr	Gly	Gln	Val	Asp	Gly	Tyr	Arg	Glu	Gly	Glu	Ile	Tyr	Phe	Pro	Gln
			100					105					110		
Ser	Pro	Leu	Leu	Thr	Val	Arg	Gly	Thr	Phe	Ala	Glu	Cys	Val	Ile	Leu
		115					120					125			
Glu	Thr	Val	Ile	Leu	Ser	Ile	Met	Asn	Ala	Asp	Ser	Ala	Val	Ala	Ser
	130					135					140				
Ala	Ala	Ala	Arg	Met	Val	Thr	Ala	Ala	Asp	Gly	Arg	Pro	Ile	Ile	Glu
145					150					155					160
Met	Gly	Ser	Arg	Arg	Thr	His	Glu	Tyr	Ser	Ala	Val	Thr	Ala	Ser	Arg
				165					170					175	
Ala	Ala	Tyr	Leu	Ala	Gly	Phe	Ser	Thr	Thr	Ser	Asn	Leu	Glu	Ala	Ala
			180					185					190		
Tyr	Arg	Tyr	Gly	Ile	Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Trp	Thr
		195				200						205			
Leu	Leu	His	Ile	Asn	Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe
	210					215					220				
Lys	Ala	Gln	Val	Glu	Ser	Leu	Gly	Val	Asp	Thr	Thr	Leu	Leu	Val	Asp
225					230					235					240
Thr	Tyr	Asp	Ile	Thr	Gln	Gly	Val	Ala	Thr	Ala	Ile	Glu	Val	Ala	Gly
			245						250					255	
Pro	Asp	Leu	Gly	Gly	Val	Arg	Ile	Asp	Ser	Gly	Asp	Leu	Gly	Val	Leu
			260					265					270		
Ala	Arg	Lys	Val	Arg	Lys	Gln	Leu	Asp	Asp	Leu	Asn	Ala	His	Asn	Thr
		275					280					285			
Lys	Ile	Val	Val	Ser	Ser	Asp	Leu	Asp	Glu	Phe	Ala	Ile	Ala	Gly	Leu

290	295	300
Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr		
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Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val		
	325	330 335
Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly		
	340	345 350
Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile		
	355	360 365
Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys		
	370	375 380
Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile		
	385	390 395 400
Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys		
	405	410 415
Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu		
	420	425 430
Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala		
	435	440 445

&lt;210&gt; 611

&lt;211&gt; 531

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(508)

&lt;223&gt; RXA02299

&lt;400&gt; 611

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				Met	Leu	Arg	Thr	Ile	
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ctc	gga	agt	aag	att	cac	cga	gcc	act	gtc	act	caa	gct	gat	cta	gat	163
Leu	Gly	Ser	Lys	Ile	His	Arg	Ala	Thr	Val	Thr	Gln	Ala	Asp	Leu	Asp	
				10				15					20			

tat	gtt	ggc	tct	gta	acc	atc	gac	gcc	gac	ctg	gtt	cac	gcc	gcc	gga	211
Tyr	Val	Gly	Ser	Val	Thr	Ile	Asp	Ala	Asp	Leu	Val	His	Ala	Ala	Gly	
			25				30					35				

ttg	atc	gaa	ggc	gaa	aaa	gtt	gcc	atc	gta	gac	atc	acc	aac	ggc	gct	259
Leu	Ile	Glu	Gly	Glu	Lys	Val	Ala	Ile	Val	Asp	Ile	Thr	Asn	Gly	Ala	
		40					45				50					

cgt	ctg	gaa	act	tat	gtc	att	gtg	ggc	gac	gcc	gga	acg	ggc	aat	att	307
Arg	Leu	Glu	Thr	Tyr	Val	Ile	Val	Gly	Asp	Ala	Gly	Thr	Gly	Asn	Ile	

55	60	65	
tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg			355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val			
70	75	80	85
atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat			403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr			
	90	95	100
gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc			451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu			
	105	110	115
ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg			499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser			
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aga agc att tagcgtttta gctcgccaat att			531
Arg Ser Ile			
135			

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35 40 45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala
50 55 60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn
65 70 75 80
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala
85 90 95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn
100 105 110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser
115 120 125
Gly Leu Leu Thr Ser Arg Ser Ile
130 135

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 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(937)

&lt;223&gt; RXA01928

&lt;400&gt; 613

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 Met Gln Val Ala Thr  
 1 5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163  
 Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly  
 10 15 20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211  
 Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val  
 25 30 35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259  
 Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val  
 40 45 50

aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307  
 Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn  
 55 60 65

tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355  
 Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly  
 70 75 80 85

gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403  
 Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly  
 90 95 100

ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451  
 Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu  
 105 110 115

ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499  
 Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala  
 120 125 130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547  
 Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys  
 135 140 145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595  
 Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp  
 150 155 160 165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643  
 Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly  
 170 175 180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691  
 Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala  
 185 190 195

caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739  
 Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys  
 200 205 210

gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787  
 Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala  
 215 220 225

agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835  
 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala  
 230 235 240 245

acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883  
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu  
 250 255 260

gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931  
 Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile  
 265 270 275

gag ctc tagtaccaac cctgcgttgc agc 960  
 Glu Leu

&lt;210&gt; 614

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His  
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His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly  
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His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val  
 35 40 45

Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys  
 50 55 60

Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu  
 65 70 75 80

Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu  
 85 90 95

Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile  
 100 105 110

Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val  
 115 120 125

Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala  
 130 135 140

Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu  
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile  
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser  
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly  
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala  
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu  
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu  
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 260 265 270

Leu Ile Asp Asn Ile Glu Leu  
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<210> 615  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(913)  
 <223> RXN01929

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 Met Pro Met Ser Gly  
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att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163  
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val  
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211  
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala  
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259  
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser  
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307  
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu  
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355  
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg  
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca	403
Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro	
90 95 100	
aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg	451
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala	
105 110 115	
gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga	499
Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg	
120 125 130	
cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc	547
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr	
135 140 145	
ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc	595
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly	
150 155 160 165	
gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg	643
Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala	
170 175 180	
ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc	691
Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg	
185 190 195	
gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc	739
Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly	
200 205 210	
aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc	787
Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu	
215 220 225	
aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc	835
Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly	
230 235 240 245	
gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg	883
Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala	
250 255 260	
ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca	933
Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe	
265 270	
aag	936

&lt;210&gt; 616

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 616

Met	Pro	Met	Ser	Gly	Ile	Asp	Ala	Lys	Lys	Ile	Arg	Thr	Arg	His	Phe
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr  
                   20                                  25                                  30  
 Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu  
                   35                                  40                                  45  
 Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr  
                   50                                  55                                  60  
 Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
                   65                                  70                                  75                                  80  
 Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
                                   85                                  90                                  95  
 Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
                                   100                                  105                                  110  
 Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
                   115                                  120                                  125  
 Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly  
                   130                                  135                                  140  
 His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val  
                   145                                  150                                  155                                  160  
 Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg  
                                   165                                  170                                  175  
 Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro  
                                   180                                  185                                  190  
 Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile  
                   195                                  200                                  205  
 Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln  
                   210                                  215                                  220  
 Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu  
                   225                                  230                                  235                                  240  
 Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile  
                                   245                                  250                                  255  
 Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
                                   260                                  265                                  270

&lt;210&gt; 617

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; FRXA01929

&lt;400&gt; 617

tgactccata acgagaactt aatcgagcaa caccctgaa cagtgaatca aatcggaatt 60

tattttattct	gagctgggtca	tcacatcttat	actcatgccc	atg	tca	ggc	att	gat	115
				Met	Ser	Gly	Ile	Asp	
				1				5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163								
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly									
	10								
	15								
	20								
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211								
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile									
	25								
	30								
	35								
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259								
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala									
	40								
	45								
	50								
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307								
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu									
	55								
	60								
	65								
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355								
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu									
	70								
	75								
	80								
	85								
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403								
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln									
	90								
	95								
	100								
gcg gtg gag tcc gcg atc ccg gtc atg cgt gaa acg ggt gcg gct gcg	451								
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala									
	105								
	110								
	115								
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499								
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile									
	120								
	125								
	130								
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547								
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln									
	135								
	140								
	145								
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595								
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser									
	150								
	155								
	160								
	165								
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643								
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala									
	170								
	175								
	180								
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691								
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val									
	185								
	190								
	195								
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739								
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly									
	200								
	205								
	210								
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787								
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg									
	215								
	220								
	225								

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835  
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser  
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883  
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr  
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930  
 Phe Pro Gly Glu Ala Glu Ser Phe  
 265

<210> 618

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu  
 1 5 10 15

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala  
 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
 225 230 235 240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
 245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 260 265

<210> 619

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

accccggcag gcaacgcctt ttccgggatt tggcgcgcag gcaggcagag atttcccgcg 60

cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115  
 Leu Ser Phe Thr His  
 1 5

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163  
 Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly  
 10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211  
 Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly  
 25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259  
 Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg  
 40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307  
 Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp  
 55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355  
 His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn  
 70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403  
 Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly  
 90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451  
 Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu  
 105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499  
 Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr  
 120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547  
 Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc			595
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala			
150	155	160	165
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca			643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala			
	170	175	180
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac			691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His			
	185	190	195
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca			739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala			
	200	205	210
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca			787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro			
	215	220	225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc			835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly			
230	235	240	245
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc			883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe			
	250	255	260
aaa aac atc gaa ggc tgatcccggt ttacccagtt cgc			921
Lys Asn Ile Glu Gly			
	265		

&lt;210&gt; 620

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln
1 5 10 15

Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val
20 25 30

Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile
35 40 45

Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala
50 55 60

Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala
65 70 75 80

Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val
85 90 95

Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr
100 105 110

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu  
115 120 125

Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn  
130 135 140

Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met  
145 150 155 160

Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp  
165 170 175

Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala  
180 185 190

His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln  
195 200 205

Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly  
210 215 220

Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala  
225 230 235 240

Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro  
245 250 255

Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly  
260 265

<210> 621

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS01145

<400> 621

taatgtagtt gtctgccc aa gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
Met Ala Ile Glu Leu  
1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
 1027  
 Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
 295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
 1075  
 Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
 310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac  
 1124  
 Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
 330 335

ccctttgacg gct  
 1137

<210> 622  
 <211> 338  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 622  
 Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
 145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
 165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
 180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205  
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220  
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240  
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255  
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270  
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285  
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300  
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
 305 310 315 320  
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335

Thr Ala

<210> 623  
 <211> 556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(556)  
 <223> FRXA01145

<400> 623  
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 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115  
 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50  
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
135 140 145

tgc ctc atc 556  
Cys Leu Ile  
150

&lt;210&gt; 624

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 624

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile  
145 150

<210> 625  
<211> 1389  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1366)  
<223> RXA02239

<400> 625  
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gtgtgggaac ccagccagcc tcttactttg aaggattgtt gtg ccc atg act cat 115  
Val Pro Met Thr His  
1 5  
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163  
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly  
10 15 20  
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211  
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu  
25 30 35  
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259  
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe  
40 45 50  
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307  
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr  
55 60 65  
acg gtg ttt gat gcg gtg gat tcg gtg cag cat gtg aaa gtt ggc cag 355  
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln  
70 75 80 85  
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403  
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala  
90 95 100  
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451  
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu  
105 110 115  
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499  
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met  
120 125 130  
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547  
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg  
135 140 145  
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595  
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp  
150 155 160 165

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc	643
Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala	
170 175 180	
aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag	691
Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys	
185 190 195	
aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg	739
Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val	
200 205 210	
cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt	787
Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly	
215 220 225	
gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat	835
Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn	
230 235 240 245	
gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg	883
Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val	
250 255 260	
tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct	931
Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser	
265 270 275	
gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg	979
Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser	
280 285 290	
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1027	
Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala	
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310 315 320 325	
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1123	
Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val	
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1171	
Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr	
345 350 355	
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1219	
Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn	
360 365 370	
gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg	
1267	
Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp	
375 380 385	

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa  
 1315  
 Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys  
 390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa  
 1363  
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 410 415 420

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 1389  
 Val

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 <212> PRT  
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 Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His  
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 85 90 95  
 Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu  
 100 105 110  
 Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala  
 115 120 125  
 Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala  
 130 135 140  
 Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg  
 145 150 155 160  
 Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln  
 165 170 175  
 Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln  
 180 185 190  
 Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu  
 195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln  
 210 215 220  
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser  
 225 230 235 240  
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu  
 245 250 255  
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 260 265 270  
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp  
 275 280 285  
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp  
 290 295 300  
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp  
 305 310 315 320  
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser  
 325 330 335  
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr  
 340 345 350  
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp  
 355 360 365  
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys  
 370 375 380  
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val  
 385 390 395 400  
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala  
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 Leu Ala Tyr Arg Glu Val  
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<220>  
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 <222> (101)..(1069)  
 <223> RXA00581

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 Met Ala Glu Gln Asn  
 1 5

gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc	163
Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe	
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agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac	211
Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn	
25 30 35	
tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc	259
Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly	
40 45 50	
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Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro	
55 60 65	
ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act	355
Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr	
70 75 80 85	
gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg	403
Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro	
90 95 100	
ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc	451
Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr	
105 110 115	
gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc	499
Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg	
120 125 130	
gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta	547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu	
135 140 145	
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Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp	
150 155 160 165	
caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc	643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu	
170 175 180	
gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca	691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro	
185 190 195	
ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc	739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly	
200 205 210	
tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc	787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe	
215 220 225	
gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg	835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp	
230 235 240 245	
tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc	883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro  
 250 255 260  
 ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931  
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile  
 265 270 275  
 gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979  
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val  
 280 285 290  
 gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa  
 1027  
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys  
 295 300 305  
 ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc  
 1069  
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile  
 310 315 320  
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 1092

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 35 40 45  
 Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala  
 50 55 60  
 Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala  
 65 70 75 80  
 Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro  
 85 90 95  
 Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val  
 100 105 110  
 Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp  
 115 120 125  
 Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr  
 130 135 140  
 Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe  
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val  
 165 170 175  
 Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala  
 180 185 190  
 Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile  
 195 200 205  
 Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met  
 210 215 220  
 Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu  
 225 230 235 240  
 Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr  
 245 250 255  
 Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala  
 260 265 270  
 Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn  
 275 280 285  
 Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser  
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 <213> Corynebacterium glutamicum

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 <223> RXS00838

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 Met Lys Ile Ala Ile  
 1 5  
 gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu  
 10 15 20  
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 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala  
 25 30 35  
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 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

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gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala 70 75 80 85			355
gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln 90 95 100			403
aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp 105 110 115			451
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro 120 125 130			499
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp 135 140 145			547
tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly 150 155 160 165			595
att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys 170 175 180			643
gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys 185 190 195			691
caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu 200 205 210			739
atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro 215 220 225			787
agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu 230 235 240 245			835
aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser 250 255 260			883
gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val 265 270 275			931
ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu 280 285 290			979

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 Lys Glu Glu Glu Asn Ser Leu  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 630  
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 20 25 30  
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 35 40 45  
 Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
 50 55 60  
 Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg  
 65 70 75 80  
 Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val  
 85 90 95  
 Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys  
 100 105 110  
 Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe  
 115 120 125  
 Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser  
 130 135 140  
 Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr  
 145 150 155 160  
 Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val  
 165 170 175  
 Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly  
 180 185 190  
 Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala  
 195 200 205  
 Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala  
 210 215 220  
 Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala  
 225 230 235 240  
 Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala  
 245 250 255

Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg  
 260 265 270

Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr  
 275 280 285

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<210> 631

<211> 408

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(385)

<223> RXC02238

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 Val Thr Asn Val Ser  
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163  
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile  
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211  
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr  
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259  
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe  
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307  
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val  
 55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355  
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile  
 70 75 80 85

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 Asn Ala Gly Leu Leu Asp His Glu Glu Gly  
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cac

408

<210> 632

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 632

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			20					25					30		
Val	Thr	Ser	Lys	Tyr	Ala	Leu	Val	Ile	Phe	Ala	Ala	Lys	Arg	Ala	Arg
		35					40					45			
Gln	Ile	Asn	Ser	Phe	Tyr	His	Gln	Ala	Asp	Glu	Gly	Val	Phe	Glu	Phe
	50					55					60				
Ile	Gly	Pro	Leu	Val	Thr	Pro	Gln	Pro	Gly	Glu	Lys	Pro	Leu	Ser	Ile
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Ala	Leu	Arg	Glu	Ile	Asn	Ala	Gly	Leu	Leu	Asp	His	Glu	Glu	Gly	
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 Val Ser Lys Leu Lys 5  
 ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163  
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala 20  
 gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211  
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu 35  
 att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259  
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala 50  
 atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307  
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu 65  
 aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355  
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val 85  
 ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403  
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu 100  
 caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451  
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln

105	110	115	
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Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile			
120	125	130	
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga			547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly			
135	140	145	
atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc			593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro			
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 35 40 45  
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
 50 55 60  
 Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
 65 70 75 80  
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
 85 90 95  
 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
 100 105 110  
 Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu  
 115 120 125  
 Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg  
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<210> 635  
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&lt;223&gt; FRXA02903

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ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163  
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala  
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gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211  
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu  
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259  
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala  
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307  
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu  
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355  
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val  
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403  
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu  
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451  
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln  
 105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499  
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile  
 120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547  
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly  
 135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593  
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro  
 150 155 160

tataaaccaa aaa 606

&lt;210&gt; 636

&lt;211&gt; 161

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 636

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly  
1 5 10 15

Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp  
20 25 30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr  
35 40 45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn  
50 55 60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly  
65 70 75 80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp  
85 90 95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile  
100 105 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu  
115 120 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg  
130 135 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys  
145 150 155 160

Pro

&lt;210&gt; 637

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(760)

&lt;223&gt; RXA00166

&lt;400&gt; 637

ggcgttttagc gatcttcaac atcgagcaac cagcgcgcagc gctttttaccc aaggcagcac 60

gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115  
Val Glu Leu Ala Arg  
1 5

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163  
Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr  
10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211  
Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp  
25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259

Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala	Val	Pro	Cys	Trp	Gln	
		40					45					50				
gcg	aca	gca	gaa	cac	aca	gga	ata	cgt	gac	aac	gcg	gtt	gat	ctg	att	307
Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn	Ala	Val	Asp	Leu	Ile	
	55					60					65					
acg	tgc	gca	caa	acg	tgg	cat	tgg	gtt	gac	gtg	acg	gct	gcc	tca	gcg	355
Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val	Thr	Ala	Ala	Ser	Ala	
	70				75					80					85	
gaa	ttt	gat	cgg	gtg	att	gca	cct	gag	ggc	gca	gtc	ctg	ctc	gtg	tgg	403
Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala	Val	Leu	Leu	Val	Trp	
				90					95					100		
aat	aac	ctg	gac	acc	tcc	atc	gcg	tgg	gta	cac	cga	ctc	agt	cgc	att	451
Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His	Arg	Leu	Ser	Arg	Ile	
			105					110					115			
atg	cat	gcc	ggc	gat	gta	ctc	aag	ccg	gga	ttc	acc	cca	gaa	acc	gca	499
Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe	Thr	Pro	Glu	Thr	Ala	
		120					125					130				
gct	ccc	tgg	ata	att	gat	cga	gaa	att	cgc	acc	acg	tgg	aat	cag	cac	547
Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr	Thr	Trp	Asn	Gln	His	
		135				140					145					
ctc	acc	cct	gaa	gaa	atc	atc	cag	ctc	gct	cac	acg	agg	tcc	tac	tgg	595
Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His	Thr	Arg	Ser	Tyr	Trp	
					155					160					165	
tta	aac	gcg	tca	gag	aaa	atc	aaa	gag	cgt	gtt	gat	cag	aac	ctt	cag	643
Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val	Asp	Gln	Asn	Leu	Gln	
				170				175						180		
tgg	tat	ctc	tac	gag	cat	ttg	ggc	ttc	agt	ccc	gac	aat	cca	gtg	gaa	691
Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro	Asp	Asn	Pro	Val	Glu	
			185				190						195			
ctt	ccc	tat	cgc	tgt	gat	gca	ttt	tta	ctt	tca	cgt	tcc	ggc	acc	ctg	739
Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser	Arg	Ser	Gly	Thr	Leu	
		200				205						210				
gca	ggc	aga	tct	tcc	aat	ctt	taggagccct	cgccatgtac	ctg							783
Ala	Gly	Arg	Ser	Ser	Asn	Leu										
	215				220											

&lt;210&gt; 638

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 638

Val	Glu	Leu	Ala	Arg	Gly	Phe	Gly	Arg	Val	Leu	Asp	Val	Gly	Ala	Gly
1				5				10					15		

Thr	Gly	Lys	Leu	Thr	Ser	Glu	Leu	Thr	Ala	Asp	Gln	Val	Leu	Ala	Leu
		20				25						30			

Asp	Pro	Ser	Met	Asp	Met	Leu	Arg	Val	Phe	Arg	Ser	Ala	Leu	Pro	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45						
Val	Pro	Cys	Trp	Gln	Ala	Thr	Ala	Glu	His	Thr	Gly	Ile	Arg	Asp	Asn	
50					55					60						
Ala	Val	Asp	Leu	Ile	Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val	
65					70					75					80	
Thr	Ala	Ala	Ser	Ala	Glu	Phe	Asp	Arg	Val	Ile	Ala	Pro	Glu	Gly	Ala	
85					90					95						
Val	Leu	Leu	Val	Trp	Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His	
100					105					110						
Arg	Leu	Ser	Arg	Ile	Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe	
115					120					125						
Thr	Pro	Glu	Thr	Ala	Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr	
130					135					140						
Thr	Trp	Asn	Gln	His	Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His	
145					150					155					160	
Thr	Arg	Ser	Tyr	Trp	Leu	Asn	Ala	Ser	Glu	Lys	Ile	Lys	Glu	Arg	Val	
165					170					175						
Asp	Gln	Asn	Leu	Gln	Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro	
180					185					190						
Asp	Asn	Pro	Val	Glu	Leu	Pro	Tyr	Arg	Cys	Asp	Ala	Phe	Leu	Leu	Ser	
195					200					205						
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210					215					220						

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00633

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 Met Glu Asn Pro Ser  
 1 5  
 ttg cgc gag ctt gat cac cga aac atc tgg cac ccg tat gcc gcg ccg 163  
 Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro  
 10 15 20  
 ggc gtg cgc aat aga ctc gtc acc aaa acc gat gga gtg ttt ttg acg 211  
 Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp Gly Val Phe Leu Thr  
 25 30 35

ctg gaa gat ggc agc acc gtg att gac gcg atg agc tcc tgg tgg tcg	259
Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met Ser Ser Trp Trp Ser	
40 45 50	
gca att cat gga cac gga cac ccc cga ctg aaa gct gcc gcc caa aaa	307
Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Ala Gln Lys	
55 60 65	
caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag	355
Gln Ile Asp Thr Met Ser His Val Met Phe Gly Gly Leu Thr His Glu	
70 75 80 85	
ccc gcc att aag ctc acc cac aaa ctc ctc aat ctc act gga aat tcc	403
Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser	
90 95 100	
ttt gac cac gtc ttt tat tcc gat tcg ggc tcg gtc tca gtg gag gtc	451
Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val	
105 110 115	
gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa	499
Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu	
120 125 130	
cgg aca aaa ctc ctc acc tgg cgg tcc ggc tac cac gga gac aca ttc	547
Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe	
135 140 145	
acc gcg atg agc gtg tgc gac cca gaa aat ggc atg cat agc ctc tgg	595
Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp	
150 155 160 165	
aaa ggc aca ctc ccc gag cag att ttc gcc ccc gcc cca cca gtt cgg	643
Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Pro Val Arg	
170 175 180	
ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg	691
Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu Arg Ser Met Glu Leu	
185 190 195	
ctt atc gac gag gcg gtc tcc gca atc atc atc gaa ccg atc gtc caa	739
Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile Glu Pro Ile Val Gln	
200 205 210	
ggc gct gga ggc atg cgc ttt cac gat gtc gca ctc att gaa gga gtc	787
Gly Ala Gly Gly Met Arg Phe His Asp Val Ala Leu Ile Glu Gly Val	
215 220 225	
gcc aca ctg tgc aag aag cac gat cgt ttc ttg atc gtc gat gaa att	835
Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu Ile Val Asp Glu Ile	
230 235 240 245	
gcc act ggt ttc ggc cgc acc ggt gaa cta ttt gcc acg tta agc aat	883
Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe Ala Thr Leu Ser Asn	
250 255 260	
ggc cta caa cca gac atc atg tgt gtg ggc aag gcc ctc acc ggt gga	931
Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly	
265 270 275	
ttc atg tcc ttc gcc gct act tta tgc acg gac aag gtg gct caa tta	979

Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu  
280 285 290

atc agc acc cca aat ggc gga ggt gcg ctg atg cac ggc ccc act ttt  
1027

Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe  
295 300 305

atg gct aat cct ctg gcc tgt gcg gtt tcg cat gct tca tta gaa atc  
1075

Met Ala Asn Pro Leu Ala Cys Ala Val Ser His Ala Ser Leu Glu Ile  
310 315 320 325

att gag acc ggc atg tgg cag aaa cag gta aaa aga atc gaa gcc gaa  
1123

Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys Arg Ile Glu Ala Glu  
330 335 340

ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat  
1171

Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp  
345 350 355

gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc  
1219

Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val  
360 365 370

aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc  
1267

Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile  
375 380 385

cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg  
1315

Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr  
390 395 400 405

tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa  
1363

Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys  
410 415 420

ggg aaa taaaccatgc cattttttatt tgt  
1392

Gly Lys

<210> 640

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His  
1 5 10 15

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp  
20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met  
 35 40 45  
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys  
 50 55 60  
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly  
 65 70 75 80  
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn  
 85 90 95  
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser  
 100 105 110  
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly  
 115 120 125  
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr  
 130 135 140  
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly  
 145 150 155 160  
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro  
 165 170 175  
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu  
 180 185 190  
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile  
 195 200 205  
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala  
 210 215 220  
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu  
 225 230 235 240  
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe  
 245 250 255  
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys  
 260 265 270  
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp  
 275 280 285  
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met  
 290 295 300  
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His  
 305 310 315 320  
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys  
 325 330 335  
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu  
 340 345 350  
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

355		360		365
Met Glu Gln Asn Val Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp				
370		375		380
His Gly Val Trp Ile Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro				
385		390		395 400
Pro Tyr Ile Thr Thr Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu				
		405		410 415
His Ala Ala Val Lys Gly Lys				
420				

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00632

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 ctgcactgcg cttcatgctg cagttaaagg gaaataaacc atg cca ttt tta ttt 115  
 Met Pro Phe Leu Phe  
 1 5  
 gtc agc ggt acc gga act ggg gtt ggg aaa acc ttc tcc aca gcc gtt 163  
 Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr Phe Ser Thr Ala Val  
 10 15 20  
 ttg gtt cga tac tta gcc gat caa gga cac gat gtt ctg ccc gta aag 211  
 Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp Val Leu Pro Val Lys  
 25 30 35  
 cta gtc caa acc ggt gaa ctt cca ggc gag gga gac atc ttt aac att 259  
 Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly Asp Ile Phe Asn Ile  
 40 45 50  
 gaa cgc ttg act gga att gct gga gag gaa ttt gct cgt ttc aaa gac 307  
 Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe Ala Arg Phe Lys Asp  
 55 60 65  
 cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata 355  
 Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu Gly Val Glu Pro Ile  
 70 75 80 85  
 cag ttt gat cag att atc tcg tgg ctt cgt ggt ttt gac gac cca gat 403  
 Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp  
 90 95 100  
 cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg gtc aga tta ggg 451  
 Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly  
 105 110 115  
 gaa gat ttc acc ctg gca gat gtt gcc tcc gct ttg aat gca ccc tta 499

Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu  
 120 125 130  
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547  
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu  
 135 140 145  
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595  
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu  
 150 155 160 165  
 ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643  
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu  
 170 175 180  
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691  
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro  
 185 190 195  
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739  
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro  
 200 205 210  
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792  
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg  
 215 220  
 tcg 795

&lt;210&gt; 642

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 642

Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr  
 1 5 10 15  
 Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp  
 20 25 30  
 Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly  
 35 40 45  
 Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe  
 50 55 60  
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu  
 65 70 75 80  
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly  
 85 90 95  
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu  
 100 105 110  
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala  
 115 120 125  
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

130		135		140
Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr				
145		150		155
Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala				
		165		170
Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe				
		180		185
Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu				
		195		200
Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg				
		210		215
				220

<210> 643  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00295

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 ttaagcgcgc agttattgac aaccagcctc taggagatcc atg acc atc ccc ggc 115  
 Met Thr Ile Pro Gly  
 1 5  
 acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163  
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly  
 10 15 20  
 ctt aat cag cag cag ttg atg gag gtt ctc acc ttg cct gaa gag caa 211  
 Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr Leu Pro Glu Glu Gln  
 25 30 35  
 atc cca gac ttg atg gaa tta gcc cac cag gtt cgg ttg aag tgg tgt 259  
 Ile Pro Asp Leu Met Glu Leu Ala His Gln Val Arg Leu Lys Trp Cys  
 40 45 50  
 ggg gaa gaa atc gag gtc gag ggc att att tcc ctc aaa act ggc ggt 307  
 Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser Leu Lys Thr Gly Gly  
 55 60 65  
 tgc cct gaa gat tgt cat ttc tgc tca cag tct ggg ttg ttt gaa tcg 355  
 Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser Gly Leu Phe Glu Ser  
 70 75 80 85  
 ccg gtg cgt tcg gtg tgg ctg gat att ccg aat ctg gtt gaa gcc gct 403  
 Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn Leu Val Glu Ala Ala  
 90 95 100

aaa	cag	acc	gca	aaa	act	ggc	gct	acc	gaa	ttc	tgt	atc	gtc	gcc	gca	451
Lys	Gln	Thr	Ala	Lys	Thr	Gly	Ala	Thr	Glu	Phe	Cys	Ile	Val	Ala	Ala	
			105					110					115			
gtc	aag	ggg	cct	gat	gag	agg	ctc	atg	acc	cag	ctg	gag	gaa	gca	gtc	499
Val	Lys	Gly	Pro	Asp	Glu	Arg	Leu	Met	Thr	Gln	Leu	Glu	Glu	Ala	Val	
		120					125					130				
ctc	gcg	att	cac	tct	gaa	gtt	gaa	att	gaa	gtc	gca	gca	tcg	atc	gga	547
Leu	Ala	Ile	His	Ser	Glu	Val	Glu	Ile	Glu	Val	Ala	Ala	Ser	Ile	Gly	
		135				140					145					
acg	tta	aat	aag	gaa	cag	gtg	gat	cgc	ctc	gct	gct	gcc	ggc	gtg	cac	595
Thr	Leu	Asn	Lys	Glu	Gln	Val	Asp	Arg	Leu	Ala	Ala	Ala	Gly	Val	His	
					155					160					165	
cgc	tac	aac	cat	aat	ttg	gaa	act	gcg	cgt	tcc	tat	ttc	cct	gaa	gtt	643
Arg	Tyr	Asn	His	Asn	Leu	Glu	Thr	Ala	Arg	Ser	Tyr	Phe	Pro	Glu	Val	
				170					175					180		
gtc	acc	act	cat	aca	tgg	gaa	gag	cgc	cgc	gaa	act	ttg	cgc	ctg	gtg	691
Val	Thr	Thr	His	Thr	Trp	Glu	Glu	Arg	Arg	Glu	Thr	Leu	Arg	Leu	Val	
			185					190					195			
gca	gaa	gct	gga	atg	gaa	gtc	tgt	tcc	ggc	gga	atc	tta	gga	atg	ggc	739
Ala	Glu	Ala	Gly	Met	Glu	Val	Cys	Ser	Gly	Gly	Ile	Leu	Gly	Met	Gly	
		200					205					210				
gaa	act	tta	gag	cag	cgc	gcc	gag	ttt	gcc	gtg	cag	ctg	gcg	gag	ctt	787
Glu	Thr	Leu	Glu	Gln	Arg	Ala	Glu	Phe	Ala	Val	Gln	Leu	Ala	Glu	Leu	
		215				220					225					
gat	ccg	cac	gaa	gtc	ccc	atg	aac	ttc	ctt	gat	cct	cgc	ccg	ggc	acc	835
Asp	Pro	His	Glu	Val	Pro	Met	Asn	Phe	Leu	Asp	Pro	Arg	Pro	Gly	Thr	
					235					240					245	
cca	ttt	gcc	gat	agg	gaa	ttg	atg	gac	agc	cgt	gac	gct	ctg	cgc	tct	883
Pro	Phe	Ala	Asp	Arg	Glu	Leu	Met	Asp	Ser	Arg	Asp	Ala	Leu	Arg	Ser	
				250					255					260		
att	ggt	gcg	ttc	cgc	ctt	gcg	atg	cct	cac	acc	atg	ctt	cgt	ttt	gct	931
Ile	Gly	Ala	Phe	Arg	Leu	Ala	Met	Pro	His	Thr	Met	Leu	Arg	Phe	Ala	
			265					270					275			
ggc	ggt	cgc	gag	ctg	act	ttg	ggc	gac	aag	ggt	tcc	gag	caa	gcc	ctc	979
Gly	Gly	Arg	Glu	Leu	Thr	Leu	Gly	Asp	Lys	Gly	Ser	Glu	Gln	Ala	Leu	
		280					285					290				
ctg	gga	ggc	atc	aat	gcg	atg	atc	gtc	gga	aac	tac	ctg	act	acg	ctc	
1027																
Leu	Gly	Gly	Ile	Asn	Ala	Met	Ile	Val	Gly	Asn	Tyr	Leu	Thr	Thr	Leu	
		295				300					305					
ggc	cgc	cca	atg	gaa	gat	gac	ctc	gac	atg	atg	gat	cgt	ctc	cag	ctg	
1075																
Gly	Arg	Pro	Met	Glu	Asp	Asp	Leu	Asp	Met	Met	Asp	Arg	Leu	Gln	Leu	
					315					320					325	
ccc	atc	aaa	gtc	ctt	aat	aag	gtc	atc	taagaagcac gcgcatgaac							
1122																

Pro Ile Lys Val Leu Asn Lys Val Ile  
330

gac  
1125

<210> 644  
<211> 334  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 644  
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20 25 30  
Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val  
35 40 45  
Arg Leu Lys Trp Cys Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser  
50 55 60  
Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser  
65 70 75 80  
Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn  
85 90 95  
Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe  
100 105 110  
Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln  
115 120 125  
Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val  
130 135 140  
Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala  
145 150 155 160  
Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser  
165 170 175  
Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu  
180 185 190  
Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly  
195 200 205  
Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val  
210 215 220  
Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp  
225 230 235 240  
Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg  
245 250 255

Asp Ala Leu Arg Ser Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr  
 260 265 270

Met Leu Arg Phe Ala Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly  
 275 280 285

Ser Glu Gln Ala Leu Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn  
 290 295 300

Tyr Leu Thr Thr Leu Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met  
 305 310 315 320

Asp Arg Leu Gln Leu Pro Ile Lys Val Leu Asn Lys Val Ile  
 325 330

&lt;210&gt; 645

&lt;211&gt; 1212

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1189)

&lt;223&gt; RXA00223

&lt;400&gt; 645

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tttgaacact ttttatctgg accatgcagc caccacacca atg cgt gag gtg gcc 115  
 Met Arg Glu Val Ala  
 1 5

gca gct gcg tgg atg gaa aac gcg cag gca ttg aat ccc gcg agt cag 163  
 Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu Asn Pro Ala Ser Gln  
 10 15 20

tac ggt tcg ggg cgt aag gcg cgc agc gtt gcg gat tcg gct cgt gaa 211  
 Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala Asp Ser Ala Arg Glu  
 25 30 35

gaa att gct tct ttg ctg ggc tgt gaa cct atc gag gtt gtg ttt acc 259  
 Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile Glu Val Val Phe Thr  
 40 45 50

gcg tcc ggc acg gag gca gat aac ctc gct gtg cag ggg tta ttc cac 307  
 Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val Gln Gly Leu Phe His  
 55 60 65

gca tcg cct ctc aat cgg att att tct acg ccg atc gag cac ccc ggg 355  
 Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro Ile Glu His Pro Gly  
 70 75 80 85

att ctg gaa acc gtc aag gct cta gaa ctt ggc ggg gca gag gcg gag 403  
 Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly Gly Ala Glu Ala Glu  
 90 95 100

ctc atg ccg atc ggt cca gat gga cga gtg tct tcc ttc gaa gcg ctg 451  
 Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser Ser Phe Glu Ala Leu  
 105 110 115

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc	499
Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr	
120 125 130	
ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc	547
Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser	
135 140 145	
ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg	595
Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro	
150 155 160 165	
gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac	643
Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His	
170 175 180	
aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca	691
Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser	
185 190 195	
cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc	739
Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile	
200 205 210	
cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca	787
Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Ala Thr Ala Ala Ala	
215 220 225	
tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc	835
Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg	
230 235 240 245	
gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac	883
Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn	
250 255 260	
gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc	931
Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu	
265 270 275	
tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc	979
Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser	
280 285 290	
ttg cgg atc gaa gcc tcc aca ggt tcg gcc tgc tcc aac ggt gta aac	
1027	
Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn	
295 300 305	
cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc	
1075	
Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala	
310 315 320 325	
cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc	
1123	
Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser	
330 335 340	
atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt	
1171	

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg  
 345 350 355

act gcg gga atg gct ttt tagcgcaccgt aaatcgcata gtg  
 1212

Thr Ala Gly Met Ala Phe  
 360

<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

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Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala  
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile  
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val  
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro  
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly  
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser  
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp  
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala  
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val  
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu  
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu  
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly  
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala  
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu  
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu

245	250	255
His Thr Ile Pro Asn Val Leu Val	His Thr Thr Glu Pro Ser Leu Pro	
260	265	270
Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile		
275	280	285
Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys		
290	295	300
Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile		
305	310	315
Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr		
325	330	335
Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val		
340	345	350
Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe		
355	360	

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1174)  
 <223> RXN00262

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 Met Leu Tyr Leu Asp  
 1 5  
 aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg 163  
 Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp  
 10 15 20  
 cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg 211  
 Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val  
 25 30 35  
 gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc 259  
 Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala  
 40 45 50  
 cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga 307  
 Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly  
 55 60 65  
 tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct 355  
 Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro  
 70 75 80 85

cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta	403
Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu	
90 95 100	
gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac	451
Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr	
105 110 115	
cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa	499
Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys	
120 125 130	
gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat	547
Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn	
135 140 145	
gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt	595
Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser	
150 155 160 165	
acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac	643
Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp	
170 175 180	
ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct	691
Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro	
185 190 195	
aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc	739
Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile	
200 205 210	
cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt	787
His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val	
215 220 225	
gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa	835
Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu	
230 235 240 245	
tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	883
Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro	
250 255 260	
gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca	931
Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala	
265 270 275	
tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg	979
Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu	
280 285 290	
gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga	
1027	
Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly	
295 300 305	
gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca	
1075	
Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala	
310 315 320 325	

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat  
 1123  
 Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
                     330                    335                    340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga  
 1171  
 Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg  
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 1197  
 Gly

<210> 648  
 <211> 358  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 648  
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 Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser  
                     20                    25                    30  
 Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala  
                     35                    40                    45  
 Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr  
                     50                    55                    60  
 Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala  
                     65                    70                    75                    80  
 Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu  
                     85                    90                    95  
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
                     100                    105                    110  
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
                     115                    120                    125  
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
                     130                    135                    140  
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu  
                     145                    150                    155                    160  
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala  
                     165                    170                    175  
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His  
                     180                    185                    190  
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro  
                     195                    200                    205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser  
 210 215 220  
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu  
 225 230 235 240  
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu  
 245 250 255  
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg  
 260 265 270  
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr  
 275 280 285  
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser  
 290 295 300  
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu  
 305 310 315 320  
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr  
 325 330 335  
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala  
 340 345 350  
 Val Ala Leu Ile Arg Gly  
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<210> 649  
 <211> 920  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (79)..(897)  
 <223> FRXA00262

<400> 649  
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 cgtgcttagc taatcctagtg gcc ggg cac ctc atc acc acc ccg atc gag 111  
 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu  
 1 5 10  
 cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159  
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp  
 15 20 25  
 ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207  
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro  
 30 35 40  
 gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255  
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile  
 45 50 55

ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303  
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu  
 60 65 70 75

gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351  
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala  
 80 85 90

cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399  
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His  
 95 100 105

aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447  
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro  
 110 115 120

ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495  
 Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser  
 125 130 135

ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543  
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu  
 140 145 150 155

ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591  
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu  
 160 165 170

gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639  
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg  
 175 180 185

att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687  
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr  
 190 195 200

gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735  
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser  
 205 210 215

gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783  
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu  
 220 225 230 235

gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831  
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr  
 240 245 250

cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879  
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala  
 255 260 265

gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920  
 Val Ala Leu Ile Arg Gly  
 270

&lt;210&gt; 650

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 650

Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu  
1 5 10 15

Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr  
20 25 30

Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys  
35 40 45

Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn  
50 55 60

Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser  
65 70 75 80

Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp  
85 90 95

Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro  
100 105 110

Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile  
115 120 125

His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val  
130 135 140

Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu  
145 150 155 160

Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro  
165 170 175

Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala  
180 185 190

Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu  
195 200 205

Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly  
210 215 220

Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala  
225 230 235 240

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp  
245 250 255

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg  
260 265 270

Gly

&lt;210&gt; 651

&lt;211&gt; 1296

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1273)

&lt;223&gt; RXN00435

&lt;400&gt; 651

cgacaggtga attcatgcac gtttgagtgt cccgtgtgtg gggtaatggt gtccaagaga 60

gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115  
 Val Gly Phe Asp Val  
 1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163  
 Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr  
 10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211  
 Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly  
 25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259  
 Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser  
 40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307  
 Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala  
 55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355  
 Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg  
 70 75 80 85

cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403  
 Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg  
 90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451  
 Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr  
 105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499  
 Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp  
 120 125 130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547  
 Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp  
 135 140 145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595  
 Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly  
 150 155 160 165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643  
 Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser  
 170 175 180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691  
 Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro  
 185 190 195

ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739  
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly  
 200 205 210

gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787  
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser  
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835  
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser  
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883  
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His  
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggc 931  
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly  
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979  
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser  
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc  
 1027  
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala  
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc  
 1075  
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe  
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac  
 1123  
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp  
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca  
 1171  
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala  
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg  
 1219  
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro  
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg  
 1267  
 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser  
 375 380 385

ctt gcc taaaccgcaa gcacgagctt gcc  
 1296  
 Leu Ala  
 390

&lt;210&gt; 652

&lt;211&gt; 391

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 652

Val	Gly	Phe	Asp	Val	Ala	Arg	Val	Arg	Gly	Leu	Tyr	Thr	Ser	Leu	Gly	1	5	10	15
Asp	Gly	Trp	Thr	Tyr	Leu	Asn	Ser	His	Gln	Ile	Pro	Gln	Val	Pro	Glu	20	25	30	
Arg	Val	Ala	Ser	Gly	Val	Ala	Ala	Ala	Phe	Arg	Thr	His	Ala	Gln	Ile	35	40	45	
Ser	Glu	Val	Thr	Ser	Gln	Pro	Ile	Ala	Val	Asp	Gln	Leu	Glu	Ala	Ala	50	55	60	
Arg	Glu	Ala	Val	Ala	Ser	Leu	Ala	Gly	Val	Asp	Pro	Asp	Cys	Val	Val	65	70	75	80
Leu	Gly	Pro	Thr	Arg	Gln	Phe	Leu	Ala	His	Thr	Leu	Ala	Arg	Gly	Leu	85	90	95	
Gly	Gly	Phe	Val	Arg	Arg	Lys	Ala	Gly	Val	Val	Leu	Ser	Arg	Ala	Asp	100	105	110	
Ala	Asp	Trp	Leu	Thr	Ala	Pro	Phe	Arg	Ser	Leu	Asp	Gly	Val	Phe	Ser	115	120	125	
Trp	Ala	Glu	Pro	Asp	Leu	Gly	Thr	Gly	Met	Leu	Pro	Asp	Trp	Gln	Tyr	130	135	140	
Glu	Lys	Leu	Val	Asp	Gly	Ser	Thr	Arg	Leu	Val	Val	Leu	Ser	Ala	Ala	145	150	155	160
His	Pro	Leu	Leu	Gly	Thr	Val	Ala	Pro	Val	Gly	Lys	Ile	Val	Asp	Lys	165	170	175	
Val	Arg	Ala	Arg	Ser	Arg	Ala	Trp	Val	Leu	Val	Asp	Ala	Thr	Thr	Tyr	180	185	190	
Ala	Ala	Tyr	Arg	Pro	Leu	Arg	Leu	Asp	Glu	Trp	Glu	Ala	Asp	Ile	Val	195	200	205	
Met	Leu	Asp	Leu	Gly	Glu	Leu	Gly	Gly	Pro	Gln	Ile	Ser	Ala	Leu	Ile	210	215	220	
Phe	Arg	Asp	Thr	Ser	Met	Phe	Pro	Arg	Leu	Asp	Arg	Thr	Val	Pro	Leu	225	230	235	240
Glu	Leu	Pro	Ala	Ser	Ser	Leu	Pro	His	Gly	Leu	Leu	Gly	Gly	Val	Pro	245	250	255	
Asn	Leu	Val	Arg	His	Leu	Gly	Asn	Leu	Asp	Glu	Asn	Ala	Pro	Ser	Val	260	265	270	
Val	Glu	Ala	Met	Gly	Glu	Met	Ala	Lys	Phe	His	Lys	Gly	Leu	Phe	Glu	275	280	285	
His	Leu	Val	Glu	Ser	Leu	Glu	Gly	Leu	His	Ala	Val	His	Ile	Val	Gly	290	295	300	

Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val  
 305 310 315 320

Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr  
 325 330 335

Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp  
 340 345 350

Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr  
 355 360 365

Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr  
 370 375 380

Arg Val Leu Ala Ser Leu Ala  
 385 390

<210> 653  
 <211> 638  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(615)  
 <223> FRXA00435

<400> 653

gtc gac gcc acc acc tac gca gcc tac cgc ccc ctg cgc cta gac gag	48
Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu	
1 5 10 15	
tg gaa gcc gat atc gtc atg ctt gat ctc ggc gag ttg ggc ggc ccg	96
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro	
20 25 30	
cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg	144
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu	
35 40 45	
gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg	192
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly	
50 55 60	
ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat	240
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp	
65 70 75 80	
gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc	288
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe	
85 90 95	
cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac	336
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His	
100 105 110	
gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc	384
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala	

115	120	125	
ccg ttc ctg gat cga gtg	ccc cgc ttg acc ttc acc atg gaa ggc gtg	432	
Pro Phe Leu Asp Arg Val	Pro Arg Leu Thr Phe Thr Met Glu Gly Val		
130	135 140		
ccc gca gat atg gtg tac	cgc cga ttg gtg gac aat cgt ttg atc act	480	
Pro Ala Asp Met Val Tyr	Arg Arg Leu Val Asp Asn Arg Leu Ile Thr		
145	150 155 160		
acc gtc agc cct gct gac	ccg ctg ctc gaa gca atg ggt gtg act gaa	528	
Thr Val Ser Pro Ala Asp	Pro Leu Leu Glu Ala Met Gly Val Thr Glu		
165	170 175		
gct ggc gga tcg atc act	atc gga cta agc ccg ttt agc acc tac tat	576	
Ala Gly Gly Ser Ile Thr	Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr		
180	185 190		
gaa gtg gat cag ctg acc	agg gtg ctg gca tcg ctt gcc taaaccgcaa	625	
Glu Val Asp Gln Leu Thr	Arg Val Leu Ala Ser Leu Ala		
195	200 205		
gcacgagctt gcc		638	

&lt;210&gt; 654

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 654

Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu	
1 5 10 15	
Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro	
20 25 30	
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu	
35 40 45	
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly	
50 55 60	
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp	
65 70 75 80	
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe	
85 90 95	
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His	
100 105 110	
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala	
115 120 125	
Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe Thr Met Glu Gly Val	
130 135 140	
Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp Asn Arg Leu Ile Thr	
145 150 155 160	

<400> 655															
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gtggaaggaa atgctgtggc ggttgaaagg agtgcctttc gtg ggt ttt gat gtg 115															
Val Gly Phe Asp Val 1 5															
gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163															
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr 10 15 20															
ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211															
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly 25 30 35															
gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259															
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser 40 45 50															
cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307															
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala 55 60 65															
tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355															
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg 70 75 80 85															
cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403															
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg 90 95 100															
cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451															
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr 105 110 115															
gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499															
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp 120 125 130															
ttg ggc acc ggc atg ctg ccg gat tgg cag tac cag 535															
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln															

135

140

145

&lt;210&gt; 656

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 656

Val Gly Phe Asp Val Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly  
 1 5 10 15

Asp Gly Trp Thr Tyr Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu  
 20 25 30

Arg Val Ala Ser Gly Val Ala Ala Phe Arg Thr His Ala Gln Ile  
 35 40 45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala  
 50 55 60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val  
 65 70 75 80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu  
 85 90 95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp  
 100 105 110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser  
 115 120 125

Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr  
 130 135 140

Gln  
 145

&lt;210&gt; 657

&lt;211&gt; 1386

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1363)

&lt;223&gt; RXA02516

&lt;400&gt; 657

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aagctcgagg ctgacggcta cgaccagttc atcaagtaac atg tcc gat ttc ctc 115  
 Met Ser Asp Phe Leu  
 1 5

aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163  
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro  
 10 15 20

atc	ctg	aag	cgc	act	gtt	agg	gat	ggg	aaa	ccg	ctt	gct	tac	ctg	gac	211
Ile	Leu	Lys	Arg	Thr	Val	Arg	Asp	Gly	Lys	Pro	Leu	Ala	Tyr	Leu	Asp	
			25					30					35			
tca	ggg	gag	aca	tcg	cag	cga	ccc	gag	cgg	gtg	tgg	cgt	gca	gag	gag	259
Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val	Trp	Arg	Ala	Glu	Glu	
		40					45					50				
cac	ttt	gtg	ctg	cac	acc	aac	gcc	ccc	gtg	cac	cgc	ggg	gcc	tac	caa	307
His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His	Arg	Gly	Ala	Tyr	Gln	
	55					60					65					
ctg	gct	gag	gaa	gca	acg	gat	gct	tat	gaa	ggg	gcc	cgc	gag	aag	atc	355
Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly	Ala	Arg	Glu	Lys	Ile	
	70				75				80						85	
gct	gcc	ttt	gtt	ggg	gcc	gag	cag	cat	gaa	att	gcg	ttc	act	aag	aat	403
Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile	Ala	Phe	Thr	Lys	Asn	
			90				95							100		
gca	act	gaa	gca	ctc	aat	ctt	gtt	gcg	tac	acc	ttg	ggg	gat	gac	cgt	451
Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr	Leu	Gly	Asp	Asp	Arg	
			105				110						115			
tcc	ggg	aag	tat	cgt	gtc	cag	gcc	ggg	gat	acc	gtg	gtc	atc	acg	gag	499
Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr	Val	Val	Ile	Thr	Glu	
		120				125						130				
cta	gag	cac	cac	gca	aac	ttg	gtg	cca	tgg	cag	gag	ctg	tgc	cgt	cga	547
Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln	Glu	Leu	Cys	Arg	Arg	
	135					140					145					
acc	ggg	gag	aca	ttg	aag	tgg	tac	aag	gtg	act	gaa	gat	ggg	cgc	att	595
Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr	Glu	Asp	Gly	Arg	Ile	
	150				155				160						165	
gat	ctc	gat	tca	ctc	gag	ctt	gat	gaa	act	gtc	aag	gtc	gtt	gcc	ttc	643
Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val	Lys	Val	Val	Ala	Phe	
			170				175							180		
act	cac	cag	tcc	aat	gtg	acc	ggg	gct	gtg	gct	gat	gtt	cca	gag	ttg	691
Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala	Asp	Val	Pro	Glu	Leu	
			185				190						195			
gtt	cgt	cgt	gcc	aag	gct	gtc	ggc	gct	ctc	acg	gtg	ctt	gat	gag	tgc	739
Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr	Val	Leu	Asp	Ala	Cys	
		200				205						210				
cag	tct	gtt	cct	cat	atg	cca	gtg	aat	ttc	cac	gag	ctg	gat	gta	gat	787
Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His	Glu	Leu	Asp	Val	Asp	
	215					220					225					
ttc	tct	gca	ttc	tct	ggc	cat	aag	atg	ctg	gga	cct	gca	ggc	gtg	ggc	835
Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly	Pro	Ala	Gly	Val	Gly	
	230				235				240					245		
gtt	gtg	tat	gca	aag	tcc	cca	atc	ttg	gat	gaa	ctg	cca	cca	ttt	ttg	883
Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu	Leu	Pro	Pro	Phe	Leu	
			250				255							260		
act	ggg	ggg	tcc	atg	att	gaa	gtt	gtc	acc	atg	gag	ggg	tcc	acc	tac	931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr  
 265 270 275

gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979  
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln  
 280 285 290

gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg  
 1027  
 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met  
 295 300 305

gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa  
 1075  
 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu  
 310 315 320 325

aag ctc acg gca att aag gga cta acc att gct ggt cct ttg act gca  
 1123  
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala  
 330 335 340

gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca  
 1171  
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro  
 345 350 355

cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc  
 1219  
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val  
 360 365 370

ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg  
 1267  
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser  
 375 380 385

aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac  
 1315  
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp  
 390 395 400 405

cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag  
 1363  
 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu  
 410 415 420

taatgaacct tgagcagatg tac  
 1386

<210> 658  
 <211> 421  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 658  
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 Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

20										25					30															
Leu	Ala	Tyr	Leu	Asp	Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val															
		35					40					45																		
Trp	Arg	Ala	Glu	Glu	His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His															
		50				55					60																			
Arg	Gly	Ala	Tyr	Gln	Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly															
		65			70					75					80															
Ala	Arg	Glu	Lys	Ile	Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile															
				85					90					95																
Ala	Phe	Thr	Lys	Asn	Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr															
			100				105						110																	
Leu	Gly	Asp	Asp	Arg	Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr															
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Val	Val	Ile	Thr	Glu	Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln															
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Glu	Leu	Cys	Arg	Arg	Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr															
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Glu	Asp	Gly	Arg	Ile	Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val															
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Lys	Val	Val	Ala	Phe	Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala															
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Asp	Val	Pro	Glu	Leu	Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr															
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Val	Leu	Asp	Ala	Cys	Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His															
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Glu	Leu	Asp	Val	Asp	Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly															
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Pro	Ala	Gly	Val	Gly	Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu															
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Leu	Pro	Pro	Phe	Leu	Thr	Gly	Gly	Ser	Met	Ile	Glu	Val	Val	Thr	Met															
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Glu	Gly	Ser	Thr	Tyr	Ala	Ala	Ala	Pro	Gln	Arg	Phe	Glu	Ala	Gly	Thr															
		275				280					285																			
Gln	Met	Thr	Ser	Gln	Val	Val	Gly	Leu	Gly	Ala	Ala	Val	Asp	Met	Leu															
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Asn	Glu	Ile	Gly	Met	Glu	Ala	Ile	Ala	Ala	His	Glu	His	Ala	Leu	Thr															
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Ala	Tyr	Ala	Leu	Glu	Lys	Leu	Thr	Ala	Ile	Lys	Gly	Leu	Thr	Ile	Ala															
				325				330						335																
Gly	Pro	Leu	Thr	Ala	Glu	Gln	Arg	Gly	Gly	Ala	Ile	Ser	Phe	Gly	Val															
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Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly  
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 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser  
 370 375 380  
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 Met Asn Leu Glu Gln  
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 atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163  
 Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys  
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 ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211  
 Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser  
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 Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser  
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 Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln  
 55 60 65  
 gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355  
 Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp  
 70 75 80 85  
 aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403  
 Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg  
 90 95 100  
 ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451  
 Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe  
 105 110 115

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499  
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly  
           120                  125                  130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547  
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His  
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<213> Corynebacterium glutamicum

<400> 660

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           20                  25                  30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu  
           35                  40                  45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly  
       50                  55                  60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val  
       65                  70                  75                  80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys  
           85                  90                  95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly  
           100                  105                  110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys  
           115                  120                  125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala  
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Val Ala His Ala His  
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<211> 1167

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<220>

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	Val Thr Ile Ala Pro	
	1 5	
gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg	163	
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro		
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att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct	211	
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro		
	25 30 35	
gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act	259	
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr		
	40 45 50	
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc	307	
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser		
	55 60 65	
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt	355	
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys		
	70 75 80 85	
gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt	403	
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly		
	90 95 100	
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac	451	
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr		
	105 110 115	
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca	499	
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala		
	120 125 130	
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac	547	
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His		
	135 140 145	
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg	595	
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu		
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ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643	
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val		
	170 175 180	
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691	
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr		
	185 190 195	
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739	
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val		
	200 205 210	
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787	
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile		
	215 220 225	

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835  
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr  
 230 235 240 245

atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883  
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg  
 250 255 260

tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931  
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu  
 265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979  
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr  
 280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa  
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 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu  
 295 300 305

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 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr  
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gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac  
 1123  
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp  
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 Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly  
 35 40 45  
 Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His  
 50 55 60  
 Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn  
 65 70 75 80  
 Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu  
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu  
 100 105 110  
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu  
 115 120 125  
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His  
 130 135 140  
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser  
 145 150 155 160  
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val  
 165 170 175  
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg  
 180 185 190  
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg  
 195 200 205  
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu  
 210 215 220  
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly  
 225 230 235 240  
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe  
 245 250 255  
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala  
 260 265 270  
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu  
 275 280 285  
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu  
 290 295 300  
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr  
 305 310 315 320  
 Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr  
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 Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn  
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&lt;210&gt; 663

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(853)

&lt;223&gt; RXA01746

&lt;400&gt; 663

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				Met	Thr	Ala	Pro	Arg	
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Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro									
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Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp									
	25 30 35								
tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat	259								
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp									
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cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc	307								
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg									
	55 60 65								
acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct	355								
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala									
	70 75 80 85								
gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc	403								
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile									
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tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta	451								
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val									
	105 110 115								
aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt	499								
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val									
	120 125 130								
gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct	547								
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala									
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cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata	595								
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile									
	150 155 160 165								
act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg	643								
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr									
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ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc	691								
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly									
	185 190 195								
ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa	739								
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu									
	200 205 210								
tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg	787								
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg									
	215 220 225								

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835  
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aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876  
 Asn Leu Pro Lys Arg Gly  
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<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

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Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn  
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr  
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu  
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro  
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp  
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val  
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly  
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala  
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile  
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly  
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp  
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp  
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Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala  
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Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly

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250

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 Met Asn Asn His Phe  
 1 5

gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc 163  
 Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr  
 10 15 20

gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc 211  
 Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu  
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gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg 259  
 Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala  
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tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gca gcg 307  
 Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala  
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 Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp  
 70 75 80 85

att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc 403  
 Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr  
 90 95 100

gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt 451  
 Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu  
 105 110 115

aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag 499  
 Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln  
 120 125 130

cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg 547  
 Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val  
 135 140 145

atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt 595  
 Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val  
 150 155 160 165

aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt ggc ggt gca 643

Asn	Glu	His	Gly	Val	Thr	Val	Val	Arg	Arg	Met	Ser	Gly	Gly	Gly	Ala		
				170					175						180		
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Met	Phe	Met	Glu	Gly	Gly	Asn	Cys	Ile	Thr	Tyr	Ser	Leu	Tyr	Ala	Pro		
			185					190					195				
gaa	tct	ctc	gtt	gct	ggc	ttg	agc	tat	gag	cag	tcc	tat	gaa	tat	ttg	739	
Glu	Ser	Leu	Val	Ala	Gly	Leu	Ser	Tyr	Glu	Gln	Ser	Tyr	Glu	Tyr	Leu		
		200					205					210					
gat	cgt	tgg	gtg	att	gct	gcg	ctg	aag	aca	cac	gat	gtt	gac	gct	tgg	787	
Asp	Arg	Trp	Val	Ile	Ala	Ala	Leu	Lys	Thr	His	Asp	Val	Asp	Ala	Trp		
	215					220					225						
tac	gtg	cct	atc	aat	gac	atc	acc	tcc	acc	ggc	gga	aaa	atc	ggc	ggc	835	
Tyr	Val	Pro	Ile	Asn	Asp	Ile	Thr	Ser	Thr	Gly	Gly	Lys	Ile	Gly	Gly		
230					235					240				245			
gct	gca	cag	aaa	cgt	cg	agt	ggc	gca	gtc	ctc	cac	cac	gtg	acc	atg	883	
Ala	Ala	Gln	Lys	Arg	Arg	Ser	Gly	Ala	Val	Leu	His	His	Val	Thr	Met		
				250					255					260			
tcc	tat	gac	atc	gat	gcg	gac	atg	atg	acc	cag	gtg	ttg	cg	att	gga	931	
Ser	Tyr	Asp	Ile	Asp	Ala	Asp	Met	Met	Thr	Gln	Val	Leu	Arg	Ile	Gly		
			265					270					275				
aag	gtg	aag	att	tcc	gac	aag	ggc	ctt	cg	agc	gca	aag	aag	cg	gtt	979	
Lys	Val	Lys	Ile	Ser	Asp	Lys	Gly	Leu	Arg	Ser	Ala	Lys	Lys	Arg	Val		
		280					285					290					
gat	cct	ctg	cg	cg	caa	aca	ggc	gca	tca	cgt	gag	caa	atc	atc	gac		
1027																	
Asp	Pro	Leu	Arg	Arg	Gln	Thr	Gly	Ala	Ser	Arg	Glu	Gln	Ile	Ile	Asp		
	295					300					305						
acc	cta	aag	tcc	aca	ttc	agt	gct	agg	tac	ggc	gcg	caa	gaa	gta	gag		
1075																	
Thr	Leu	Lys	Ser	Thr	Phe	Ser	Ala	Arg	Tyr	Gly	Ala	Gln	Glu	Val	Glu		
310					315					320					325		
ctc	agc	gat	gaa	gat	ttc	gcg	gca	ggc	cac	gac	cta	gta	aaa	acc	aaa		
1123																	
Leu	Ser	Asp	Glu	Asp	Phe	Ala	Ala	Gly	His	Asp	Leu	Val	Lys	Thr	Lys		
				330					335					340			
tac	gcc	acc	gag	gag	tgg	act	aag	cga	gtt	caa	tag	ttt	ctat	ggat	ctgcac		
1176																	
Tyr	Ala	Thr	Glu	Glu	Trp	Thr	Lys	Arg	Val	Gln							
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1179

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<211> 352

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val  
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 Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser  
 20 25 30  
 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg  
 35 40 45  
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala  
 50 55 60  
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly  
 65 70 75 80  
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly  
 85 90 95  
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val  
 100 105 110  
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln  
 115 120 125  
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp  
 130 135 140  
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile  
 145 150 155 160  
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met  
 165 170 175  
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr  
 180 185 190  
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln  
 195 200 205  
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His  
 210 215 220  
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly  
 225 230 235 240  
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu  
 245 250 255  
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln  
 260 265 270  
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser  
 275 280 285  
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg  
 290 295 300  
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly  
 305 310 315 320  
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp



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Asp Glu Pro Leu Leu Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile		
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Pro Ser Pro Val Ala Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp		
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Asp Thr Val Asp Val Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp		
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1282)  
 <223> RXS01260

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 Val Thr Phe Asn Tyr  
 1 5  
 gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163  
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly  
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 ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211  
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly  
 25 30 35  
 ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259  
 Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys  
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 gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307  
 Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly  
 55 60 65  
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 Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val  
 70 75 80 85  
 tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403  
 Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val  
 90 95 100  
 att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451  
 Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly

105						110						115						
aac	tac	ggt	gta	gat	gta	acc	gtc	atc	gag	ttc	atg	gat	cgt	gtg	ctt			499
Asn	Tyr	Gly	Val	Asp	Val	Thr	Val	Ile	Glu	Phe	Met	Asp	Arg	Val	Leu			
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cca	aat	gaa	gat	gct	gaa	gtc	tcc	aag	gtt	att	gca	aag	gcc	tac	aag			547
Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile	Ala	Lys	Ala	Tyr	Lys			
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aag	atg	ggc	gtt	aag	ctt	ctt	cct	ggc	cat	gca	acc	act	gct	gtt	cgg			595
Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala	Thr	Thr	Ala	Val	Arg			
		150			155					160					165			
gac	aac	ggt	gac	ttt	gtc	gag	gtt	gat	tac	cag	aag	aag	ggc	tct	gac			643
Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln	Lys	Lys	Gly	Ser	Asp			
				170					175					180				
aag	aca	gag	act	ctt	act	gtt	gat	cga	gtc	atg	gtt	tcc	gtt	ggg	ttc			691
Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met	Val	Ser	Val	Gly	Phe			
			185					190					195					
cgt	cca	cgc	gtt	gag	gga	ttt	ggg	ctt	gaa	aac	act	ggc	gtt	aag	ctc			739
Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn	Thr	Gly	Val	Lys	Leu			
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acc	gag	cgt	ggc	gca	atc	gag	atc	gat	gat	tac	atg	cgt	acc	aac	gtc			787
Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr	Met	Arg	Thr	Asn	Val			
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gat	ggc	att	tac	gcc	atc	ggg	gac	gtg	acc	gcc	aag	ctt	cag	ctt	gct			835
Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala	Lys	Leu	Gln	Leu	Ala			
		230			235					240					245			
cac	gtc	gca	gaa	gca	cag	ggc	att	gtt	gcc	gca	gag	act	att	gct	ggg			883
His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala	Glu	Thr	Ile	Ala	Gly			
				250					255					260				
gca	gaa	act	cag	act	ctt	ggg	gat	tac	atg	atg	atg	cca	cgt	gca	acc			931
Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met	Met	Pro	Arg	Ala	Thr			
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ttc	tgc	aac	cca	cag	gtt	tct	tcc	ttt	ggg	tac	acc	gaa	gag	cag	gcc			979
Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr	Thr	Glu	Glu	Gln	Ala			
		280					285					290						
aag	gag	aag	tgg	cca	gat	cgt	gag	atc	aag	gtt	gct	tcc	ttc	cca	ttc			
1027																		
Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val	Ala	Ser	Phe	Pro	Phe			
		295				300					305							
tct	gca	aac	ggg	aaa	gca	gtt	ggc	ctg	gca	gaa	act	gat	ggg	ttc	gca			
1075																		
Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu	Thr	Asp	Gly	Phe	Ala			
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310																		
aag	atc	gtt	gct	gat	gca	gaa	ttc	ggg	gag	ctg	ctc	ggg	gca	cac	ctg			
1123																		
Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu	Leu	Gly	Ala	His	Leu			
				330					335					340				

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag  
 1171  
 Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln  
                   345                                  350                                  355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac  
 1219  
 Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His  
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cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga  
 1267  
 Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly  
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 His Met Ile Asn Phe  
 390

<210> 670  
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 <213> Corynebacterium glutamicum

<400> 670  
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                   20                                  25                                  30  
 Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu  
                   35                                  40                                  45  
 Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys  
                   50                                  55                                  60  
 Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe  
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 Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala  
                                   85                                  90                                  95  
 Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe  
                   100                                  105                                  110  
 Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe  
                   115                                  120                                  125  
 Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile  
                   130                                  135                                  140  
 Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala  
   145                                  150                                  155                                  160  
 Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln  
                   165                                  170                                  175  
 Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

180								185				190			
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn
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Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr
210								215				220			
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala
225								230				235			
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala
245								250				255			
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met
260								265				270			
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr
275								280				285			
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val
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Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu
305								310				315			
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu
325								330				335			
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu
340								345				350			
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg
355								360				365			
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala
370								375				380			
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe						
385								390							

&lt;210&gt; 671

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(271)

&lt;223&gt; RXS01261

&lt;400&gt; 671

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				Val	Thr	Glu	His	Tyr	
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gac	gta	gta	gta	ctc	gga	gcc	ggc	ccc	ggc	tat	gtc	tcc	gcc	atc	163
Asp	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ser	Ala	Ile

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cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac				211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr				
	25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct				259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser				
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Asp Gln Lys Arg				
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Pro Ser Lys Val Ser Asp Gln Lys Arg	
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 <213> Corynebacterium glutamicum

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	Met Pro Pro Arg Asp
	1 5
gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac	163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp	
	10 15 20
ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc	211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr	
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cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg	259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu	

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acc	act	ctg	gtg	cac	ctg	acc	ctg	gtt	aac	cac	act	cgc	gaa	gag	atg	307		
Thr	Thr	Leu	Val	His	Leu	Thr	Leu	Val	Asn	His	Thr	Arg	Glu	Glu	Met			
	55					60					65							
aag	gca	att	ctt	cgg	gaa	tac	cta	gag	ctg	gga	tta	aca	aac	ctg	ttg	355		
Lys	Ala	Ile	Leu	Arg	Glu	Tyr	Leu	Glu	Leu	Gly	Leu	Thr	Asn	Leu	Leu			
70					75					80					85			
gcg	ctt	cga	gga	gat	ccg	cct	gga	gac	cca	tta	ggc	gat	tgg	gtg	agc	403		
Ala	Leu	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Leu	Gly	Asp	Trp	Val	Ser			
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acc	gat	gga	gga	ctg	aac	tat	gcc	tct	gag	ctc	atc	gat	ctt	att	aag	451		
Thr	Asp	Gly	Gly	Leu	Asn	Tyr	Ala	Ser	Glu	Leu	Ile	Asp	Leu	Ile	Lys			
			105					110					115					
tcc	act	cct	gag	ttc	cgg	gaa	ttc	gac	ctc	ggt	atc	gcc	tcc	ttc	ccc	499		
Ser	Thr	Pro	Glu	Phe	Arg	Glu	Phe	Asp	Leu	Gly	Ile	Ala	Ser	Phe	Pro			
		120					125					130						
gaa	ggg	cat	ttc	cgg	gcg	aaa	act	cta	gaa	gaa	gac	acc	aaa	tac	act	547		
Glu	Gly	His	Phe	Arg	Ala	Lys	Thr	Leu	Glu	Glu	Asp	Thr	Lys	Tyr	Thr			
	135					140					145							
ctg	gcg	aag	ctg	cgt	gga	ggg	gca	gag	tac	tcc	atc	acg	cag	atg	ttc	595		
Leu	Ala	Lys	Leu	Arg	Gly	Gly	Ala	Glu	Tyr	Ser	Ile	Thr	Gln	Met	Phe			
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Phe	Asp	Val	Glu	Asp	Tyr	Leu	Arg	Leu	Arg	Asp	Arg	Leu	Val	Ala	Ala			
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gac	ccc	att	cat	ggt	gcg	aag	cca	atc	att	cct	ggc	atc	atg	ccc	att	691		
Asp	Pro	Ile	His	Gly	Ala	Lys	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile			
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Leu	Pro	Ser	Gln	Leu	Glu	Glu	Ser	Leu	Val	Arg	Ala	Ala	Asn	Gly	Asn			
	215					220					225							
gaa	gaa	gcg	aac	aaa	gac	gag	atc	cgc	aag	gtg	ggc	att	gaa	tat	tcc	835		
Glu	Glu	Ala	Asn	Lys	Asp	Glu	Ile	Arg	Lys	Val	Gly	Ile	Glu	Tyr	Ser			
230					235					240					245			
acc	aat	atg	gca	gag	cga	ctc	att	gcc	gaa	ggt	gcg	gaa	gat	ctg	cac	883		
Thr	Asn	Met	Ala	Glu	Arg	Leu	Ile	Ala	Glu	Gly	Ala	Glu	Asp	Leu	His			
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Phe	Met	Thr	Leu	Asn	Phe	Thr	Arg	Ala	Thr	Gln	Glu	Val	Leu	Tyr	Asn			
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ctt	ggc	atg	gcg	cct	gct	tgg	gga	gca	gag	cac	ggc	caa	gac	gcg	gtg	979		
Leu	Gly	Met	Ala	Pro	Ala	Trp	Gly	Ala	Glu	His	Gly	Gln	Asp	Ala	Val			
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1005  
Arg

<210> 674  
<211> 294  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 674

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Ala	Gly	Gly	Ser	Thr	Arg	Glu	Arg	Thr	Ser	Arg	Ile	Ala	Arg	Arg	Leu			
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Ala	Lys	Gln	Pro	Leu	Thr	Thr	Leu	Val	His	Leu	Thr	Leu	Val	Asn	His			
	50					55					60							
Thr	Arg	Glu	Glu	Met	Lys	Ala	Ile	Leu	Arg	Glu	Tyr	Leu	Glu	Leu	Gly			
65					70					75					80			
Leu	Thr	Asn	Leu	Leu	Ala	Leu	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Leu			
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Gly	Asp	Trp	Val	Ser	Thr	Asp	Gly	Gly	Leu	Asn	Tyr	Ala	Ser	Glu	Leu			
			100					105					110					
Ile	Asp	Leu	Ile	Lys	Ser	Thr	Pro	Glu	Phe	Arg	Glu	Phe	Asp	Leu	Gly			
		115					120					125						
Ile	Ala	Ser	Phe	Pro	Glu	Gly	His	Phe	Arg	Ala	Lys	Thr	Leu	Glu	Glu			
	130					135					140							
Asp	Thr	Lys	Tyr	Thr	Leu	Ala	Lys	Leu	Arg	Gly	Gly	Ala	Glu	Tyr	Ser			
145					150					155					160			
Ile	Thr	Gln	Met	Phe	Phe	Asp	Val	Glu	Asp	Tyr	Leu	Arg	Leu	Arg	Asp			
			165						170					175				
Arg	Leu	Val	Ala	Ala	Asp	Pro	Ile	His	Gly	Ala	Lys	Pro	Ile	Ile	Pro			
			180					185					190					
Gly	Ile	Met	Pro	Ile	Thr	Ser	Leu	Arg	Ser	Val	Arg	Arg	Gln	Val	Glu			
		195					200					205						
Leu	Ser	Gly	Ala	Gln	Leu	Pro	Ser	Gln	Leu	Glu	Glu	Ser	Leu	Val	Arg			
	210					215					220							
Ala	Ala	Asn	Gly	Asn	Glu	Glu	Ala	Asn	Lys	Asp	Glu	Ile	Arg	Lys	Val			
225					230					235					240			
Gly	Ile	Glu	Tyr	Ser	Thr	Asn	Met	Ala	Glu	Arg	Leu	Ile	Ala	Glu	Gly			
				245					250					255				

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln  
                   260                                  265                                  270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His  
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Gly Gln Asp Ala Val Arg  
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&lt;210&gt; 675

&lt;211&gt; 601

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(601)

&lt;223&gt; RXN02027

&lt;400&gt; 675

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   Met Ser Gln Thr Lys  
   1                                  5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163  
   Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu  
                                   10                                  15                                  20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211  
   Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr  
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tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259  
   Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val  
                                   40                                  45                                  50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307  
   Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu  
                                   55                                  60                                  65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355  
   Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp  
                                   70                                  75                                  80                                  85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403  
   Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly  
                                   90                                  95                                  100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451  
   Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe  
                                   105                                  110                                  115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499  
   Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile  
                                   120                                  125                                  130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547  
   Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595  
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp  
 150 155 160 165

gat atc 601  
 Asp Ile

<210> 676  
 <211> 167  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 676  
 Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg  
 1 5 10 15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile  
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala  
 35 40 45

Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp  
 50 55 60

Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu  
 65 70 75 80

Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val  
 85 90 95

Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro  
 100 105 110

Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys  
 115 120 125

Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg  
 130 135 140

Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn  
 145 150 155 160

Gly Glu Ile Arg Asp Asp Ile  
 165

<210> 677  
 <211> 595  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(595)  
 <223> FRXA02027

&lt;400&gt; 677

tcacgtgctc atcgataggc aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60

tcgtcgtacc cctccgaaaa taacgggttat ccttagattt atg agc caa act aag 115  
 Met Ser Gln Thr Lys  
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163  
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu  
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211  
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr  
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259  
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val  
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307  
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu  
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355  
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp  
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403  
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly  
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451  
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe  
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499  
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile  
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547  
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly  
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595  
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp  
 150 155 160 165

&lt;210&gt; 678

&lt;211&gt; 165

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg  
 1 5 10 15

Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile  
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala

35	40	45
Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp		
50	55	60
Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu		
65	70	75
Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val		
85	90	95
Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro		
100	105	110
Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys		
115	120	125
Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg		
130	135	140
Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn		
145	150	155
Gly Glu Ile Arg Asp		
165		

<210> 679  
 <211> 579  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(556)  
 <223> RXA00106

<400> 679  
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 gctacgatcc acacccattg atccgcggca aggtcgccgt atg atc ggt gcg att 115  
 Met Ile Gly Ala Ile  
 1 5  
 tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163  
 Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro  
 10 15 20  
 tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211  
 Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly  
 25 30 35  
 cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259  
 Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys  
 40 45 50  
 ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307  
 Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly  
 55 60 65  
 gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly  
 70 75 80 85  
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403  
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala  
 90 95 100  
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451  
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr  
 105 110 115  
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499  
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu  
 120 125 130  
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547  
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr  
 135 140 145  
 atc aag gtt taaggagcaa acaacatgag caa 579  
 Ile Lys Val  
 150

&lt;210&gt; 680

&lt;211&gt; 152

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 680

Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp  
 1 5 10 15  
 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys  
 20 25 30  
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu  
 35 40 45  
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser  
 50 55 60  
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
 65 70 75 80  
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
 85 90 95  
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
 100 105 110  
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
 115 120 125  
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr  
 130 135 140  
 Lys Phe Gln Arg Tyr Ile Lys Val  
 145 150

<400> 681															
ggaggggtgta gtcaaggatt tgggccatgg tggagcggga aatcgtcata tccataccct 60															
acttagacct gacttagtgt gggaaaattt ccagggtaga atg caa cga atg acc 115															
Met Gln Arg Met Thr 1 5															
ccg agt tct cct gaa gtt cgt aat cgt ccg agc gct gcg cct gaa gag 163															
Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser Ala Ala Pro Glu Glu 10 15 20															
cgt cag ttt gtg ctc act ttt ggc tgc cct gac tcc act gga att gtg 211															
Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp Ser Thr Gly Ile Val 25 30 35															
gcg aag ttg tcg tcg ttc cta gct gag cgt ggg ggt tgg att act gag 259															
Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly Gly Trp Ile Thr Glu 40 45 50															
gct gga tat ttc acg gat cct gat tcg aat tgg ttc ttt act cgt cag 307															
Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp Phe Phe Thr Arg Gln 55 60 65															
gcg att cgc gct gag tcg att gat acc acg att gag cag ttg cgg gag 355															
Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile Glu Gln Leu Arg Glu 70 75 80 85															
gag ttc gct ccg ctt gcg gag gag ttc ggc ccg agg gct aag tgg agt 403															
Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro Arg Ala Lys Trp Ser 90 95 100															
ttc act gac act gcg cag gtg aag aag gct gtg ttg ttg gtg tct aag 451															
Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val Leu Leu Val Ser Lys 105 110 115															
gag ggc cac tgc ttg cac gat ttg tta ggt cgt gtg gct gag aat gat 499															
Glu Gly His Cys Leu His Asp Leu Leu Gly Arg Val Ala Glu Asn Asp 120 125 130															
tat ccg atg gaa gtt gtt gcg gtt gtg ggt aac cat gag aac ttg cgt 547															
Tyr Pro Met Glu Val Val Ala Val Val Gly Asn His Glu Asn Leu Arg 135 140 145															
tat att gcg gag aac cat aat gtt ccg ttt ttc cat gtg ccg ttt cct 595															
Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe His Val Pro Phe Pro 150 155 160 165															
aag gat gcg gtt ggt aag cgg aag gcg ttt gac cag gtc gct gag att 643															
Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile 170 175 180															

gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691  
Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln  
185 190 195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739  
Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn  
200 205 210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787  
Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His  
215 220 225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835  
Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr  
230 235 240 245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883  
Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile  
250 255 260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931  
Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg  
265 270 275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979  
Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu  
280 285 290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat  
1021  
Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp  
295 300 305

taaggctttt tgcttttcga cgc  
1044

<210> 682  
<211> 307  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 682  
Met Gln Arg Met Thr Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser  
1 5 10 15  
Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp  
20 25 30  
Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly  
35 40 45  
Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp  
50 55 60  
Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile  
65 70 75 80  
Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro  
85 90 95

Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val  
 100 105 110  
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg  
 115 120 125  
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn  
 130 135 140  
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe  
 145 150 155 160  
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp  
 165 170 175  
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu  
 180 185 190  
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala  
 195 200 205  
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly  
 210 215 220  
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
 225 230 235 240  
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
 245 250 255  
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met  
 260 265 270  
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu  
 275 280 285  
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val  
 290 295 300  
 Val Phe Asp  
 305

<210> 683  
 <211> 582  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (23) .. (559)  
 <223> FRXA01321

<400> 683  
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 Val Ala Glu Asn Asp Tyr Pro Met Glu Val  
 1 5 10  
 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100  
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn  
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148  
 His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly  
                   30                  35                  40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196  
 Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp  
                   45                  50                  55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244  
 Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp  
                   60                  65                  70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292  
 Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe  
                   75                  80                  85                  90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340  
 Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg  
                   95                  100                  105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388  
 Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu  
                   110                  115                  120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436  
 Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys  
                   125                  130                  135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484  
 Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln  
                   140                  145                  150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532  
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val  
                   155                  160                  165                  170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579  
 Tyr Gly Asn Arg Thr Val Val Phe Asp  
                   175

cgc 582

&lt;210&gt; 684

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 684

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn  
   1                  5                  10                  15

His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe  
                   20                  25                  30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp  
                   35                  40                  45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu  
                   50                  55                  60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala  
65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly  
85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly  
100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile  
115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met  
130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu  
145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val  
165 170 175

Val Phe Asp

<210> 685  
<211> 975  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(952)  
<223> RXA00461

<400> 685  
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tgattgtaag gccttggaag aggggtggaat aatagcgggc gtg act gca atc aaa 115  
Val Thr Ala Ile Lys  
1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163  
Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln  
10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211  
Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr  
25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259  
Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys  
40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307  
His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu  
55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355  
Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct	Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro	403		
	90	95	100	
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag	Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys	451		
	105	110	115	
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac	Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn	499		
	120	125	130	
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg	Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu	547		
	135	140	145	
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc	Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly	595		
	150	155	160	165
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt	Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg	643		
	170	175	180	
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg	Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu	691		
	185	190	195	
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag	Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln	739		
	200	205	210	
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc	Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu	787		
	215	220	225	
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac	Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His	835		
	230	235	240	245
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc	Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly	883		
	250	255	260	
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc	Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg	931		
	265	270	275	
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg	Ala Glu Lys Leu Ala Gly Leu	975		
	280			

&lt;210&gt; 686

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 686

Val Thr Ala Ile Lys Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe  
 1 5 10 15  
 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val  
 20 25 30  
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser  
 35 40 45  
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser  
 50 55 60  
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala  
 65 70 75 80  
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val  
 85 90 95  
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg  
 100 105 110  
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly  
 115 120 125  
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly  
 130 135 140  
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys  
 145 150 155 160  
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu  
 165 170 175  
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr  
 180 185 190  
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile  
 195 200 205  
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro  
 210 215 220  
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu  
 225 230 235 240  
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser  
 245 250 255  
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His  
 260 265 270  
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu  
 275 280

&lt;210&gt; 687

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(688)

&lt;223&gt; RXA01514

&lt;400&gt; 687

accacagaaa tgcctgtcgt tccagatcag cccatcgatg gtgattccgg gaagtccgct 60

gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115  
 Val Asp Asn His Ala  
 1 5

gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163  
 Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ile Arg Glu  
 10 15 20

ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211  
 Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu  
 25 30 35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259  
 Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu  
 40 45 50

cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307  
 His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His  
 55 60 65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355  
 Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu  
 70 75 80 85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403  
 His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro  
 90 95 100

ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451  
 Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala  
 105 110 115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499  
 Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln  
 120 125 130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547  
 Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val  
 135 140 145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595  
 Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys  
 150 155 160 165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643  
 Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn  
 170 175 180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688  
 Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His  
 185 190 195

taaatgaacg tatcctcttt gac 711

<210> 688  
 <211> 196  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 688

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Val Asp Asn His Ala Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr
  1              5              10              15

Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg
          20              25              30

Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu
          35              40              45

Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
      50              55              60

Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
  65              70              75              80

Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
          85              90              95

Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
          100              105              110

Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
          115              120              125

Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala
      130              135              140

Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met
  145              150              155              160

Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg
          165              170              175

Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu
          180              185              190

Ile Arg Gly His
      195
  
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<210> 689  
 <211> 513  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(490)

<223> RXA01516

<400> 689

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gttgatgttg ccgcattgtg gcgaagtgga ggaactcacc atg gct gat cgt att 115
  
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<400> 690
Met Ala Asp Arg Ile Glu Leu Lys Gly Leu Glu Cys Phe Gly His His
   1                               5               10              15
Gly Val Phe Asp Phe Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp
                20                      25                  30
Val Thr Cys Trp Met Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu
          35                          40                   45
Ser Asp Thr Val Asp Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile
    50                        55                            60
Val Glu Gly Pro Ser Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser
   65                                70                     75             80
Ala Asp Ala Val Met Ala Lys Phe Asp Ala Leu His Ala Val Glu Val
                              85                         90              95
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Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val  
 100 105 110

Ala Val Val Ala Arg Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser  
 115 120 125

Asn Ala  
 130

<210> 691

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA01515

<400> 691

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ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115  
 Met Asn Val Ser Ser  
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163  
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr  
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211  
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala  
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259  
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp  
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307  
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser  
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355  
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala  
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403  
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala  
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451  
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu  
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499  
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val  
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys	Leu	Met	His	Trp	Arg	Thr	Leu	Gln	Phe	Gly	Asp	Ala	Ala	Gly	Gln	
135						140					145					
gca	gat	cac	ggt	gga	gac	gtt	gta	gcc	gat	gtg	cac	gca	gtg	ctt	gat	595
Ala	Asp	His	Gly	Gly	Asp	Val	Val	Ala	Asp	Val	His	Ala	Val	Leu	Asp	
150					155					160					165	
gat	ctt	gtc	gcc	cgc	gcc	acc	gct	gct	ggt	gtg	gcc	gaa	aac	cag	atc	643
Asp	Leu	Val	Ala	Arg	Ala	Thr	Ala	Ala	Gly	Val	Ala	Glu	Asn	Gln	Ile	
				170					175					180		
gtg	ctt	gat	cca	ggt	ttg	ggt	ttt	gcc	aaa	tca	cgt	gaa	gac	aac	tgg	691
Val	Leu	Asp	Pro	Gly	Leu	Gly	Phe	Ala	Lys	Ser	Arg	Glu	Asp	Asn	Trp	
			185					190					195			
cgt	ttg	ctg	caa	gca	ctg	ccc	gag	ttt	att	tct	gga	cct	ttc	ccc	atc	739
Arg	Leu	Leu	Gln	Ala	Leu	Pro	Glu	Phe	Ile	Ser	Gly	Pro	Phe	Pro	Ile	
		200					205					210				
ctg	gtg	gga	gca	tcc	cgg	aag	cga	ttc	ctg	gct	ggc	gtg	cgc	aaa	gac	787
Leu	Val	Gly	Ala	Ser	Arg	Lys	Arg	Phe	Leu	Ala	Gly	Val	Arg	Lys	Asp	
	215					220					225					
cgt	ggc	cta	gat	gtc	acc	ccc	att	gat	gcc	gac	cca	gca	acc	gca	gcg	835
Arg	Gly	Leu	Asp	Val	Thr	Pro	Ile	Asp	Ala	Asp	Pro	Ala	Thr	Ala	Ala	
230					235					240					245	
gtg	acc	gca	gtg	tct	gca	cat	atg	gga	gca	tgg	ggt	gtg	cgc	gtg	cac	883
Val	Thr	Ala	Val	Ser	Ala	His	Met	Gly	Ala	Trp	Gly	Val	Arg	Val	His	
				250				255						260		
gat	gtc	cca	gta	tca	agg	gac	gct	gtt	gat	gtt	gcc	gca	ttg	tgg	cga	931
Asp	Val	Pro	Val	Ser	Arg	Asp	Ala	Val	Asp	Val	Ala	Ala	Leu	Trp	Arg	
			265					270					275			
agt	gga	gga	act	cac	cat	ggc	tgatcgtatt	gaacttaaag	gcc							975
Ser	Gly	Gly	Thr	His	His	Gly										
		280														

&lt;210&gt; 692

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 692

Met	Asn	Val	Ser	Ser	Leu	Thr	Ile	Pro	Gly	Arg	Cys	Leu	Val	Met	Gly	
1				5					10					15		
Ile	Val	Asn	Val	Thr	Glu	Asp	Ser	Phe	Ser	Asp	Gly	Gly	Lys	Tyr	Ile	
			20					25					30			
Asp	Val	Asp	Gln	Ala	Ile	Ala	His	Ala	Lys	Glu	Leu	Val	Ala	Ala	Gly	
		35				40						45				
Ala	Asp	Met	Ile	Asp	Val	Gly	Gly	Glu	Ser	Thr	Arg	Pro	Gly	Ala	Val	
	50					55				60						
Arg	Val	Asp	Ala	Ser	Val	Glu	Arg	Asp	Arg	Val	Val	Pro	Val	Ile	Lys	
65					70					75					80	

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala  
85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp  
100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu  
115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly  
130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val  
145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val  
165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser  
180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser  
195 200 205

Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala  
210 215 220

Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp  
225 230 235 240

Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp  
245 250 255

Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val  
260 265 270

Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly  
275 280

&lt;210&gt; 693

&lt;211&gt; 859

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(859)

&lt;223&gt; RXA02024

&lt;400&gt; 693

cactgatgac ctggatcagg ccgtcaaatt catcgctgat gcacacgctg gattggacgt 60

agcgcgtctc cacaattaag cagtggctac attaggtgtt atg agt tct ttg ccg 115  
Met Ser Ser Leu Pro  
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163  
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys  
10 15 20

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc	211
Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val	
25 30 35	
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc	259
Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly	
40 45 50	
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca	307
Pro Gly Asp Phe Val Ser Ala Glu Glu Ile Asp Arg Val Val Pro	
55 60 65	
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt	355
Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val	
70 75 80 85	
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca	403
Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala	
90 95 100	
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag	451
Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln	
105 110 115	
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg	499
Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly	
120 125 130	
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg	547
Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val	
135 140 145	
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt	595
Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg	
150 155 160 165	
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc	643
Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe	
170 175 180	
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag	691
Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu	
185 190 195	
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat	739
Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp	
200 205 210	
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc	787
Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly	
215 220 225	
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt	835
Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe	
230 235 240 245	
cgc gtg cat gaa gtt gcg gaa acc	859
Arg Val His Glu Val Ala Glu Thr	
250	

<210> 694  
 <211> 253  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 694  
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 Ser Phe Tyr Asp Lys Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn  
                   20                  25                  30  
 Arg Ala Ala Glu Val Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly  
                   35                  40                  45  
 Gly Val Lys Ala Gly Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile  
           50                  55                  60  
 Asp Arg Val Val Pro Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp  
   65                  70                  75                  80  
 Ile Asp Ile Ser Val Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala  
                   85                  90                  95  
 Val Ala His Gly Ala Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp  
                   100                  105                  110  
 His Glu Leu Val Gln Val Ala Gly Gln His Lys Val Gly Tyr Val Cys  
           115                  120                  125  
 Ser His Thr Gly Gly Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His  
   130                  135                  140  
 Phe Asp Asp Ile Val Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala  
 145                  150                  155                  160  
 Glu Gln Ala Val Arg Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp  
                   165                  170                  175  
 Pro Thr His Asp Phe Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu  
                   180                  185                  190  
 Arg Arg Ile Asp Glu Val Val Ala Thr Gly Trp Pro Val Leu Met Ala  
           195                  200                  205  
 Leu Ser Asn Lys Asp Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp  
   210                  215                  220  
 Lys Arg Val Ala Gly Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg  
 225                  230                  235                  240  
 Gly Val Ala Ala Phe Arg Val His Glu Val Ala Glu Thr  
                   245                  250

<210> 695  
 <211> 579  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>

<221> CDS  
 <222> (101)..(556)  
 <223> RXA00106

<400> 695

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                Met Ile Gly Ala Ile
                1                    5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
                10                    15                    20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
                25                    30                    35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
                40                    45                    50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
                55                    60                    65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
                70                    75                    80                    85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
                90                    95                    100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
                105                    110                    115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
                120                    125                    130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
                135                    140                    145

atc aag gtt taaggagcaa acaacatgag caa 579
Ile Lys Val
150

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<210> 696  
 <211> 152  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 696

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Met Ile Gly Ala Ile Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp
  1                    5                    10                    15

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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys  
                     20                    25                    30  
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu  
                     35                    40                    45  
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser  
                     50                    55                    60  
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
                     65                    70                    75                    80  
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
                     85                    90                    95  
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
                     100                    105                    110  
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
                     115                    120                    125  
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr  
                     130                    135                    140  
 Lys Phe Gln Arg Tyr Ile Lys Val  
 145                    150

<210> 697  
 <211> 1556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1533)  
 <223> RXA00989

<400> 697  
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 Gly Ile Gly Leu Val Ala Asn Asn Asp Gly Ile Phe Asp Ser Glu Asn  
           1                    5                    10                    15  
 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96  
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser  
                     20                    25                    30  
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144  
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu  
                     35                    40                    45  
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192  
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu  
                     50                    55                    60  
 gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240  
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met  
                     65                    70                    75                    80  
 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288  
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

85								90					95					
att	cac	gtg	gct	ggc	acc	aac	ggt	aag	acc	tcc	acc	acc	cgc	atg	atc	336		
Ile	His	Val	Ala	Gly	Thr	Asn	Gly	Lys	Thr	Ser	Thr	Thr	Arg	Met	Ile			
			100					105					110					
gag	tcg	ttg	ctg	cgc	gca	ttc	cac	cgc	cgc	acc	ggc	cgg	acc	acc	agc	384		
Glu	Ser	Leu	Leu	Arg	Ala	Phe	His	Arg	Arg	Thr	Gly	Arg	Thr	Thr	Ser			
		115					120					125						
ccg	cac	ctg	cag	ctg	gta	acc	gaa	cgc	atc	gcg	att	gat	ggc	aag	ccc	432		
Pro	His	Leu	Gln	Leu	Val	Thr	Glu	Arg	Ile	Ala	Ile	Asp	Gly	Lys	Pro			
		130				135					140							
atc	cac	ccg	cgt	gat	ttc	gtg	cgg	atc	tac	gaa	gag	att	aag	ccc	tac	480		
Ile	His	Pro	Arg	Asp	Phe	Val	Arg	Ile	Tyr	Glu	Glu	Ile	Lys	Pro	Tyr			
					150					155					160			
atg	gag	atg	acc	gac	gcc	tgg	tca	gag	gcc	gag	ggc	gga	ccg	aag	atg	528		
Met	Glu	Met	Thr	Asp	Ala	Trp	Ser	Glu	Ala	Glu	Gly	Gly	Pro	Lys	Met			
				165					170					175				
agc	aag	ttt	gag	gca	ctc	gtg	gcc	ctc	gct	tac	gca	ggc	ttt	gcc	gac	576		
Ser	Lys	Phe	Glu	Ala	Leu	Val	Ala	Leu	Ala	Tyr	Ala	Gly	Phe	Ala	Asp			
			180					185					190					
gct	cct	gtt	gac	gtc	gcc	gtc	gtt	gag	gtt	ggc	ctt	ggc	gga	cgc	tgg	624		
Ala	Pro	Val	Asp	Val	Ala	Val	Val	Glu	Val	Gly	Leu	Gly	Gly	Arg	Trp			
		195					200					205						
gat	gcc	act	aac	gtg	atc	aac	gca	gct	gtt	tcc	gtg	atc	acc	ccg	gtg	672		
Asp	Ala	Thr	Asn	Val	Ile	Asn	Ala	Ala	Val	Ser	Val	Ile	Thr	Pro	Val			
		210				215					220							
ggc	atg	gac	cac	gtg	gat	cgc	ctg	ggc	aac	acc	att	ggc	gaa	atc	gct	720		
Gly	Met	Asp	His	Val	Asp	Arg	Leu	Gly	Asn	Thr	Ile	Gly	Glu	Ile	Ala			
		225			230					235					240			
ggc	gaa	aag	gcc	ggc	atc	atc	aag	gct	cgt	cct	gca	tct	gag	gat	ggc	768		
Gly	Glu	Lys	Ala	Gly	Ile	Ile	Lys	Ala	Arg	Pro	Ala	Ser	Glu	Asp	Gly			
			245					250						255				
acc	gag	cct	gag	ggc	aac	gtt	gtc	atc	gtg	ggc	aag	cag	gag	cca	gaa	816		
Thr	Glu	Pro	Glu	Gly	Asn	Val	Val	Ile	Val	Gly	Lys	Gln	Glu	Pro	Glu			
			260					265					270					
gca	atg	aac	gtg	att	ctg	cag	caa	gcc	gtg	gac	gtg	gac	gca	gct	gtt	864		
Ala	Met	Asn	Val	Ile	Leu	Gln	Gln	Ala	Val	Asp	Val	Asp	Ala	Ala	Val			
		275					280					285						
gct	cgt	ttg	aac	atg	gaa	ttc	ggc	gtg	gtg	gaa	tcc	gcc	att	gcc	gtt	912		
Ala	Arg	Leu	Asn	Met	Glu	Phe	Gly	Val	Val	Glu	Ser	Ala	Ile	Ala	Val			
		290				295					300							
ggc	gga	cag	cag	ctc	acc	ctg	aag	ggc	gtg	ggc	ggc	gaa	tac	acc	gac	960		
Gly	Gly	Gln	Gln	Leu	Thr	Leu	Lys	Gly	Leu	Gly	Gly	Glu	Tyr	Thr	Asp			
		305			310					315					320			
atc	ttc	ctc	cca	ctg	tct	ggc	gcg	cac	caa	gca	gat	aat	gcc	gcg	gtt			
1008																		
Ile	Phe	Leu	Pro	Leu	Ser	Gly	Ala	His	Gln	Ala	Asp	Asn	Ala	Ala	Val			

	325		330		335
gct ctc gca gca gtg gaa gca ttt ttc ggt gca tcc gcc gga cgc cca					
1056					
Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro					
	340		345		350
ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca					
1104					
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro					
	355		360		365
ggt cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca					
1152					
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala					
	370		375		380
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt					
1200					
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg					
	385		390		395
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac					
1248					
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp					
	405		410		415
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa					
1296					
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu					
	420		425		430
att gtg tgc acc cag act gcc tca gag cgc gca ttg gac gca tac gat					
1344					
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp					
	435		440		445
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc					
1392					
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val					
	450		455		460
caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa					
1440					
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu					
	465		470		475
gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc					
1488					
Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile					
	485		490		495
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca					
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Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala					
	500		505		510
tgagcaagcg tgaagaatca att					
1556					

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 698

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Asp	Asp	Ile	Thr	Val	Gly	Asp	Val	Thr	Leu	Gly	Glu	Thr	Gly	Leu	Ser
			20					25					30		
Leu	Pro	Ile	Asp	Leu	Ala	Gly	Glu	Val	Glu	Ala	Pro	Ala	Ser	Glu	Glu
		35					40					45			
Ile	Thr	Gln	Glu	Asp	Leu	Leu	Arg	Leu	Ala	Gln	Val	Glu	Ala	Glu	Leu
	50					55					60				
Asp	Gln	Arg	Trp	Leu	Glu	Thr	Lys	Ile	Asp	Pro	Thr	Phe	Arg	Arg	Met
65					70					75					80
Ser	Tyr	Met	Met	Asp	Leu	Met	Gly	Gln	Pro	Gln	Asn	Ser	Phe	Pro	Ala
				85					90					95	
Ile	His	Val	Ala	Gly	Thr	Asn	Gly	Lys	Thr	Ser	Thr	Thr	Arg	Met	Ile
			100					105					110		
Glu	Ser	Leu	Leu	Arg	Ala	Phe	His	Arg	Arg	Thr	Gly	Arg	Thr	Thr	Ser
		115					120					125			
Pro	His	Leu	Gln	Leu	Val	Thr	Glu	Arg	Ile	Ala	Ile	Asp	Gly	Lys	Pro
		130				135					140				
Ile	His	Pro	Arg	Asp	Phe	Val	Arg	Ile	Tyr	Glu	Glu	Ile	Lys	Pro	Tyr
145					150					155					160
Met	Glu	Met	Thr	Asp	Ala	Trp	Ser	Glu	Ala	Glu	Gly	Gly	Pro	Lys	Met
				165					170					175	
Ser	Lys	Phe	Glu	Ala	Leu	Val	Ala	Leu	Ala	Tyr	Ala	Gly	Phe	Ala	Asp
			180					185					190		
Ala	Pro	Val	Asp	Val	Ala	Val	Val	Glu	Val	Gly	Leu	Gly	Gly	Arg	Trp
		195					200					205			
Asp	Ala	Thr	Asn	Val	Ile	Asn	Ala	Ala	Val	Ser	Val	Ile	Thr	Pro	Val
	210					215					220				
Gly	Met	Asp	His	Val	Asp	Arg	Leu	Gly	Asn	Thr	Ile	Gly	Glu	Ile	Ala
225					230					235					240
Gly	Glu	Lys	Ala	Gly	Ile	Ile	Lys	Ala	Arg	Pro	Ala	Ser	Glu	Asp	Gly
				245					250					255	
Thr	Glu	Pro	Glu	Gly	Asn	Val	Val	Ile	Val	Gly	Lys	Gln	Glu	Pro	Glu
			260					265					270		
Ala	Met	Asn	Val	Ile	Leu	Gln	Gln	Ala	Val	Asp	Val	Asp	Ala	Ala	Val
		275					280					285			
Ala	Arg	Leu	Asn	Met	Glu	Phe	Gly	Val	Val	Glu	Ser	Ala	Ile	Ala	Val

290					295					300					
Gly	Gly	Gln	Gln	Leu	Thr	Leu	Lys	Gly	Leu	Gly	Gly	Glu	Tyr	Thr	Asp
305					310					315					320
Ile	Phe	Leu	Pro	Leu	Ser	Gly	Ala	His	Gln	Ala	Asp	Asn	Ala	Ala	Val
				325					330					335	
Ala	Leu	Ala	Ala	Val	Glu	Ala	Phe	Phe	Gly	Ala	Ser	Ala	Gly	Arg	Pro
				340				345					350		
Leu	Asp	Ile	Asp	Thr	Val	Arg	Glu	Gly	Phe	Ala	Gln	Val	Gln	Ser	Pro
		355					360					365			
Gly	Arg	Leu	Glu	Arg	Leu	Arg	Ser	Ala	Pro	Thr	Val	Phe	Ile	Asp	Ala
		370				375					380				
Ala	His	Asn	Pro	His	Gly	Ala	Ala	Ala	Leu	Gly	Ala	Ala	Leu	Asp	Arg
385					390					395					400
Asp	Phe	Glu	Phe	Arg	Arg	Leu	Ile	Gly	Val	Ile	Gly	Val	Leu	Cys	Asp
				405					410					415	
Lys	Asp	Ala	Arg	Gly	Ile	Leu	Glu	Ser	Leu	Glu	Pro	Tyr	Leu	His	Glu
			420					425					430		
Ile	Val	Cys	Thr	Gln	Thr	Ala	Ser	Glu	Arg	Ala	Leu	Asp	Ala	Tyr	Asp
		435					440					445			
Leu	Ala	Glu	Tyr	Ala	Arg	Glu	Ile	Tyr	Gly	Asp	Glu	Arg	Val	His	Val
		450				455					460				
Gln	Glu	Asp	Leu	Ala	Gly	Ala	Val	Glu	Leu	Ala	Ile	Glu	Leu	Ala	Glu
465					470					475					480
Asp	Thr	Asp	Val	Gln	Ser	Gly	Ser	Gly	Val	Val	Ile	Thr	Gly	Ser	Ile
				485					490					495	
Val	Thr	Ala	Gly	Asp	Ala	Arg	Thr	Leu	Phe	Gly	Lys	Glu	Pro	Ala	
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&lt;211&gt; 600

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(577)

&lt;223&gt; RXA01517

&lt;400&gt; 699

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				Met	His	Ala	Val	Leu	
				1				5	

tcc	atc	ggt	tcc	aac	atg	gat	gat	cgc	tac	gcg	ctg	ctc	aac	aca	gtg	163
Ser	Ile	Gly	Ser	Asn	Met	Asp	Asp	Arg	Tyr	Ala	Leu	Leu	Asn	Thr	Val	

	10	15	20	
atc gag gaa ttc aaa gat gag atc gtg gcg cag tct gcg atc tac tca				211
Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser				
	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val				
	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly				
	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly				
	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu				
	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala				
	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp				
	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp				
	135	140	145	
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat				597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile				
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gca				600

&lt;210&gt; 700

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 700

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Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln				
	20	25	30	
Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu				
	35	40	45	
Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu				
	50	55	60	
Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg				
	65	70	75	80

Val Arg Lys Trp Gly Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile  
                                   85                                  90                                  95

Ile Lys Asp Gly Glu Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu  
                                   100                                  105                                  110

Pro His Pro Trp Ala Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu  
                                   115                                  120                                  125

Glu Ala Glu Pro Asp Ala Val Leu His Gly Thr Thr Ile Ala Glu His  
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Val Asp Asn Leu Asp Pro Thr Asp Ile Glu Gly Val Thr Lys Ile  
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<220>  
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   Met Arg Val Leu Ile  
   1                                  5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163  
 Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu  
                                   10                                  15                                  20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211  
 Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile  
                                   25                                  30                                  35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259  
 Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His  
                                   40                                  45                                  50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307  
 Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg  
                                   55                                  60                                  65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355  
 Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala  
                                   70                                  75                                  80                                  85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403  
 Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly  
                                   90                                  95                                  100

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451  
 Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile  
                                   105                                  110                                  115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc	499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg	
120 125 130	
ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc	547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile	
135 140 145	
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat	595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His	
150 155 160 165	
ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
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Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	
ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa	
1027	
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	
1075	
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
310 315 320 325	
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct	
1123	
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
330 335 340	

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat  
 1171  
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr  
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg  
 1219  
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser  
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc  
 1267  
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala  
 375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat  
 1315  
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr  
 390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg  
 1363  
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro  
 410 415 420

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc  
 1411  
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro  
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa  
 1459  
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu  
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg  
 1507  
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu  
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc  
 1555  
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro  
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca  
 1603  
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr  
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt  
 1651  
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser  
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt  
 1699  
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly  
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct  
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala  
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc  
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly  
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat  
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn  
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
600 605 610

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1983

Leu Phe Gly Val Glu Phe Pro  
615 620

<210> 702

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

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Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
 130 135 140  
 Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
 145 150 155 160  
 Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
 165 170 175  
 Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
 180 185 190  
 Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
 195 200 205  
 Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln  
 210 215 220  
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys  
 225 230 235 240  
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp  
 245 250 255  
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp  
 260 265 270  
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala  
 275 280 285  
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg  
 290 295 300  
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu  
 305 310 315 320  
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val  
 325 330 335  
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
 340 345 350  
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
 370 375 380  
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala  
 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
 420 425 430  
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
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 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

450		455		460
Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala				
465		470		475
Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val				
	485		490	495
Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu				
	500		505	510
Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly				
	515		520	525
Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp				
	530		535	540
Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr				
	545		550	555
Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu				
	565		570	575
Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu				
	580		585	590
Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser				
	595		600	605
Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro				
	610		615	620

&lt;210&gt; 703

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(724)

&lt;223&gt; RXA00958

&lt;400&gt; 703

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                                   Met Thr His Val Val
                                   1                      5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc      163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
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gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg      211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
                                   25                      30                      35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga      259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
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 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala  
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ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691  
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile  
 185 190 195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744  
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tca 747

&lt;210&gt; 704

&lt;211&gt; 208

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 704

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Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg  
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Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
 35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80  
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95  
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110  
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125  
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His  
 130 135 140  
 Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr  
 145 150 155 160  
 Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp  
 165 170 175  
 Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro  
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 <213> Corynebacterium glutamicum

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 Met Glu Pro Val Tyr  
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 Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile  
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 Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg  
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 Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val  
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gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa	307
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Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser	
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aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	
90 95 100	
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Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	
105 110 115	
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Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	
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gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	
135 140 145	
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Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu	
150 155 160 165	
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Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	
170 175 180	
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Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys	
185 190 195	
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc	739
Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	
200 205 210	
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac	787
Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	
215 220 225	
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	835
His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	
230 235 240 245	
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	883
Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala	
250 255 260	
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Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	
265 270 275	
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	979
Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	
280 285 290	

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1027  
Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr  
295 300 305

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1075  
Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala  
310 315 320 325

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Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly  
330 335 340

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1171  
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345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac  
1219  
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1266  
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<211> 381  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 706  
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Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly  
35 40 45  
Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu  
50 55 60  
Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe  
65 70 75 80  
Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly  
85 90 95  
Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala  
100 105 110  
Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly  
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly  
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 Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn  
 145 150 155 160  
 Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro  
 165 170 175  
 Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg  
 180 185 190  
 Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr  
 195 200 205  
 Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile  
 210 215 220  
 Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala  
 225 230 235 240  
 Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu  
 245 250 255  
 Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val  
 260 265 270  
 Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr  
 275 280 285  
 Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp  
 290 295 300  
 Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro  
 305 310 315 320  
 Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu  
 325 330 335  
 Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350  
 Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
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 370 375 380

&lt;210&gt; 707

&lt;211&gt; 579

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;222&gt; (101)..(556)

&lt;223&gt; RXA00106

&lt;400&gt; 707

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50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu  
65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala  
85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr  
100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe  
115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr  
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Lys Phe Gln Arg Tyr Ile Lys Val  
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<210> 709

<211> 2599

<212> DNA

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<220>

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<223> RXN02198

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Met Ser Thr Ser Val  
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163  
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala  
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211  
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu  
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259  
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly  
40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307  
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355  
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr  
70 75 80 85

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Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

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cct gag cac atc cgt gcg gtc -cgc gat gcg gtg gtt ggt gtt cca gag 1075 Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu 310 315 320 325			

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag  
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 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln  
 330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc  
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 345 350 355

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 1267  
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly  
 375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt  
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 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly  
 390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc  
 1363  
 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr  
 410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg  
 1411  
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 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp  
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 1603  
 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln  
 490 495 500

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 1651  
 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp  
 505 510 515

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1699  
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp  
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat  
1747  
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp  
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca  
1795  
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro  
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac  
1843  
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn  
570 575 580

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1891  
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile  
585 590 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg  
1939  
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro  
600 605 610

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1987  
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val  
615 620 625

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2035  
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln  
630 635 640 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa  
2083  
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu  
650 655 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc  
2131  
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile  
665 670 675

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2179  
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys  
680 685 690

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2227  
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met  
695 700 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc  
 2275  
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe  
 710 715 720 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa  
 2323  
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu  
 730 735 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag  
 2371  
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu  
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ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat  
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 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp  
 760 765 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac  
 2467  
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp  
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 2515  
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala  
 790 795 800 805

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 2563  
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 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile  
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 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr  
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Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
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Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
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Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
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Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
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Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
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